

Query= 51-11-3-D5-CL1_3C
(99 letters)

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens
113,759 sequences; 24,820,038 total letters

Searching.....done

Sequences producing significant alignments:			Score (bits)	E Value
GSP:Y35928	Y35928	Extended human secreted protein sequence, SEQ...	214	4e-56
GSP:Y36054	Y36054	Extended human secreted protein sequence, SEQ...	210	5e-55
GSP:Y12791	Y12791	Human 5' EST secreted protein SEQ ID NO:381.	170	5e-43
GSP:R81936	R81936	Human ITI-K1 Kunitz domain derived protein DK...	57	8e-09
SP:P02760	P02759	P00977 AMBP_HUMAN AMBP PROTEIN PRECURSOR [CONT...	54	7e-08
GSP:R92237	R92237	Human wild-type urinary trypsin inhibitor. >G...	54	7e-08
GSP:R78553	R78553	Human ITI Kunitz domain 1. >GSP:W64115 W64115...	54	7e-08
GSP:R99217	R99217	Inter alpha trypsin inhibitor (ITI) light chain.	54	7e-08
GSP:P81110	P81110	Sequence of new fusion protein contg. alpha-1...	54	7e-08
STR:P78491	P78491	ALPHA-1-MICROGLOBULIN (FRAGMENT). >GNP:X54818...	54	7e-08
GSP:W69522	W69522	rUTI protein SEQ ID NO:24 from WO9829453 Clai...	54	7e-08
GSP:R99157	R99157	Human aprotinin-like Kunitz domain (ITI-D1).	53	9e-08
GSP:R92233	R92233	Human mature urinary trypsin inhibitor with m...	53	1e-07
GSP:R92235	R92235	Human urinary trypsin inhibitor with modified...	53	1e-07
GSP:R92238	R92238	Human UTI modified kunitz domain 1 and flanki...	53	1e-07
GSP:W25929	W25929	Anti-trypsin inhibitor UTI Kunitz domain 1.	52	3e-07
GSP:R81915	R81915	LACI Kunitz domain LACI-K2 derived protein DK...	52	4e-07
GSP:W61536	W61536	Human tissue factor pathway inhibitor-2 (TFPI...	52	4e-07
SP:P48307	TFP2_HUMAN	TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSO...	52	4e-07
GSP:R42309	R42309	LAC1 gene product.	51	5e-07
GSP:R81921	R81921	Human TFPI-2 domain 3 Kunitz domain derived p...	51	5e-07
GSP:R92231	R92231	Human urinary trypsin inhibitor modified kuni...	51	6e-07
GSP:W00017	W00017	TFPI chimeric protein.	50	1e-06
GSP:R92265	R92265	TFPI mutein, Lys36Arg.	50	1e-06
GSP:R92011	R92011	Ubiquitin-TFPI fusion protein.	50	1e-06
GSP:W47435	W47435	Aprotinin variant 4.	50	1e-06
STR:O95103	O95103	TISSUE FACTOR PATHWAY INHIBITOR BETA. >GNP:AF...	50	1e-06
GSP:W30311	W30311	Recombinant non-glycosylated TFPI. >GSP:W6153...	50	1e-06
GSP:Y70273	Y70273	Human tissue factor pathway inhibitor protein...	50	1e-06
GSP:R39802	R39802	TFPI 2. >GSP:R81914 R81914 Lipoprotein-associ...	50	1e-06
GSP:Y70272	Y70272	Human mutant tissue factor pathway inhibitor ...	50	1e-06
RTR:CAA01311	CAA01311	KUNITZ-TYPE PROTEASE INHIBITOR. >GNP:A170...	50	1e-06
GSP:R23799	R23799	LACI fragment 90 - 160.	50	1e-06
SP:P10646	TFPI_HUMAN	TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR ...	50	1e-06
GSP:R23800	R23800	LACI fragment 1 - 160.	50	1e-06
GSP:P92002	P92002	Human tissue factor inhibitor (TFI).	50	1e-06
GSP:R81933	R81933	Human HKI B9 domain Kunitz domain derived pro...	49	2e-06
GSP:R81919	R81919	Human collagen alpha-3 Kunitz domain derived ...	49	2e-06
GSP:R92258	R92258	TFPI-2 first Kunitz-type domain.	49	2e-06
GSP:R92259	R92259	TFPI second Kunitz-type domain.	49	2e-06
GSP:R74976	R74976	Generic human Kunitz-type protease-inhibitor.	49	2e-06
GSP:R78547	R78547	Human TFPI-2 domain 1 Kunitz domain. >GSP:R81...	49	2e-06
GSP:R81899	R81899	Kallikrein inhibitor protein KKI/3(b).	48	3e-06
GSP:W47432	W47432	Aprotinin variant 1.	48	3e-06
GSP:Y70010	Y70010	Human Protease and associated protein-4 (PPRG...	48	4e-06
GSP:R78389	R78389	Human lipoprotein-associated coagulation inhi...	48	4e-06
GSP:R81917	R81917	LACI Kunitz domain LACI-K3 derived protein DK...	48	4e-06
STR:AAG00547	AAG00547	Eppin-2. >GNP:AF286369 AF286369_1 Homo sa...	48	4e-06
GSP:W75219	W75219	Human secreted protein encoded by gene 24 clo...	48	4e-06
GSP:R22979	R22979	Aprotinin analogue #4 with reduced nephrotoxi...	48	5e-06
GSP:R39673	R39673	C-terminal Kunitz-type protease inhibitor var...	48	5e-06
GSP:R22985	R22985	Aprotinin analogue #10 with reduced nephrotox...	48	5e-06
GSP:W47434	W47434	Aprotinin variant 3.	48	5e-06
GSP:R22983	R22983	Aprotinin analogue #8 with reduced nephrotoxi...	48	5e-06
GSP:W47433	W47433	Aprotinin variant 2.	47	7e-06
GSP:R39677	R39677	C-terminal Kunitz-type protease inhibitor var...	47	9e-06
GSP:R81898	R81898	Kallikrein inhibitor protein KKI/3(a).	47	9e-06
GSP:R81907	R81907	Kallikrein inhibitor protein KK2/#6.	47	9e-06
GSP:R81897	R81897	Kallikrein inhibitor protein KKII/3#10.	47	9e-06
GSP:R39672	R39672	C-terminal Kunitz-type protease inhibitor var...	46	1e-05
GSP:W47436	W47436	Aprotinin variant 5.	46	1e-05
GSP:Y68039	Y68039	Kunitz protease inhibitor analogue protein se...	46	2e-05
GSP:Y68148	Y68148	Kunitz protease inhibitor variant TW177.	46	2e-05
GSP:R39676	R39676	C-terminal Kunitz-type protease inhibitor var...	46	2e-05
GSP:W19801	W19801	Alpha mating factor:KPI(-4-57;I16H,S17F) enco...	46	2e-05

SP:P49223	KIB9_HUMAN	KUNITZ-TYPE PROTEASE INHIBITOR HKIB9 (FRAG...	46	2e-05
GSP:R22984	R22984	Aprotinin analogue #9 with reduced nephrotoxi...	46	2e-05
GSP:R39678	R39678	C-terminal Kunitz-type protease inhibitor var...	46	2e-05
GSP:W30060	W30060	Human consensus bikunin.	46	2e-05
GSP:W30045	W30045	Human placental bikunin.	46	2e-05
GSP:W30043	W30043	Human placental bikunin.	46	2e-05
GSP:W30040	W30040	Human placental bikunin. >GSP:W13665 W13665 H...	46	2e-05
STR:O43291	O43291	HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR ...	46	2e-05
GSP:R81932	R81932	Human HKI B9 domain Kunitz domain. >GSP:R9920...	46	2e-05
STR:Q9UJG4	Q9UJG4	DJ461P17.8 (HKIB7 (KUNITZ/BOVINE PANCREATIC T...	46	2e-05
RTR:CAA01298	CAA01298	KUNITZ TYPE PROTEASE INHIBITOR. >RTR:E974...	46	2e-05
GSP:W30044	W30044	Human consensus bikunin.	46	2e-05
GSP:Y68147	Y68147	Kunitz protease inhibitor variant TW176.	46	2e-05
SP:P12111	Q16501	CA36_HUMAN COLLAGEN ALPHA 3(VI) CHAIN PRECURSO...	45	3e-05
GSP:R47542	R47542	Sequence of the last 70 AAs of the C5 domain ...	45	3e-05
GSP:R81908	R81908	Kallikrein inhibitor protein KK2/#10.	45	3e-05
SP:Q02388	CA17_HUMAN	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LON...	45	4e-05
GSP:R78545	R78545	Human collagen alpha-3 Kunitz domain. >GSP:R8...	45	4e-05
GSP:R81926	R81926	Human TFPI-2 domain 3 Kunitz domain derived p...	45	4e-05
GSP:R81909	R81909	Kallikrein inhibitor protein KK2/#8.	45	4e-05
GSP:W19802	W19802	Alpha mating factor:KPI(-4-57;I16H,S17Y) enco...	45	4e-05
GSP:Y68040	Y68040	Kunitz protease inhibitor analogue protein se...	45	4e-05
STR:Q14054	Q14054	COLLAGEN TYPE VII PRECURSOR. >GNP:L23982 L239...	45	4e-05
GNP:L06862	L06862_1	Human type VII collagen (COL7A1) mRNA, 3' e...	45	4e-05
SP:Q06481	APP2_HUMAN	AMYLOID-LIKE PROTEIN 2 PRECURSOR (AMYLOID ...	45	5e-05
GSP:R39674	R39674	C-terminal Kunitz-type protease inhibitor var...	45	5e-05
GSP:R39666	R39666	Human TFPI kunitz-type domain 1-yeast signal ...	45	5e-05
GSP:R53776	R53776	Sequence of human Kunitz-type inhibitor.	45	5e-05
GSP:R53778	R53778	Sequence of human amyloid protein precursor h...	45	5e-05
PIR:A54849	PH0844	S16316 I56328 A30296 I84686 A54849 collagen a...	45	5e-05
STR:AAD47291	AAD47291	Amyloid precursor protein homolog HSD-2. ...	45	5e-05
STR:Q14594	Q14594	BINDING PROTEIN (FRAGMENT). >GNP:L23113 L2311...	45	5e-05
STR:O14895	O14895	KUNITZ-TYPE PROTEASE INHIBITOR. >GNP:AF027205...	45	5e-05
GSP:R81889	R81889	Kallikrein inhibitor protein KKII/3#2.	44	6e-05
GSP:R22988	R22988	Aprotinin analogue #13 with reduced nephrotox...	44	6e-05
GSP:R22986	R22986	Aprotinin analogue #11 with reduced nephrotox...	44	6e-05
GSP:W19803	W19803	Alpha mating factor:KPI(-4-57;I16H,S17W) enco...	44	6e-05
GSP:W64143	W64143	Human Kunitz-type serine protease inhibitor d...	44	6e-05
GSP:Y68041	Y68041	Kunitz protease inhibitor analogue protein se...	44	6e-05
STR:O95959	O95959	DJ461P17.1 PROTEIN (FRAGMENT).	44	6e-05
GSP:R22987	R22987	Aprotinin analogue #12 with reduced nephrotox...	44	8e-05
GSP:R22989	R22989	Aprotinin analogue #14 with reduced nephrotox...	44	8e-05
GSP:R39670	R39670	C-terminal Kunitz-type protease inhibitor var...	44	8e-05
GSP:R81931	R81931	Human protease nexin-II Kunitz domain derived...	44	8e-05
GSP:R81905	R81905	Kallikrein inhibitor protein KK2/#1.	44	8e-05
GSP:W64145	W64145	Human Kunitz-type serine protease inhibitor d...	44	8e-05
GSP:R81890	R81890	Kallikrein inhibitor protein KKII/3#3.	44	8e-05
GSP:R39664	R39664	Human TFPI kunitz-type protease inhibitor dom...	43	1e-04
GSP:R81903	R81903	Kallikrein inhibitor protein KK2/#5. >GSP:R81...	43	1e-04
GSP:R92257	R92257	TFPI first Kunitz-type domain.	43	1e-04
GSP:W19805	W19805	Alpha mating factor:KPI(-4-57;M15L,I16H) enco...	43	1e-04
GSP:W18411	W18411	KPI(-4 to 57) I16H. >GSP:Y68075 Y68075 Kunitz...	43	1e-04
GSP:W64123	W64123	Human Kunitz-type serine protease inhibitor d...	43	1e-04
GSP:W64129	W64129	Human Kunitz-type serine protease inhibitor d...	43	1e-04
GSP:Y68044	Y68044	Kunitz protease inhibitor analogue protein se...	43	1e-04
PIR:S41082	S41082	amyloid precursor protein homolog - human (fr...	43	1e-04
GSP:W19804	W19804	Alpha mating factor:KPI(-4-57;M15A,I16H) enco...	43	2e-04
GSP:W64147	W64147	Human Kunitz-type serine protease inhibitor d...	43	2e-04
GSP:W64126	W64126	Human Kunitz-type serine protease inhibitor d...	43	2e-04
GSP:Y68043	Y68043	Kunitz protease inhibitor analogue protein se...	43	2e-04
GSP:Y68146	Y68146	Kunitz protease inhibitor variant DD170.	43	2e-04
GSP:Y68176	Y68176	Kunitz protease inhibitor variant DD118.	43	2e-04
GSP:R22981	R22981	Aprotinin analogue #6 with reduced nephrotoxi...	43	2e-04
GSP:R22982	R22982	Aprotinin analogue #7 with reduced nephrotoxi...	42	2e-04
GSP:W18431	W18431	KPI(-4 to 57) I16H, G38Y. >GSP:Y68140 Y68140 ...	42	2e-04
GSP:W30053	W30053	Human placental bikunin.	42	2e-04
GSP:W30054	W30054	Human placental bikunin.	42	2e-04
GSP:W30041	W30041	Human placental bikunin.	42	2e-04
GSP:W30042	W30042	Human placental bikunin.	42	2e-04
GSP:W30046	W30046	Human placental bikunin.	42	2e-04
GSP:W30047	W30047	Human placental bikunin.	42	2e-04
GSP:W27368	W27368	Hepatocyte growth factor activator inhibitor....	42	2e-04
GSP:W30051	W30051	Human placental bikunin.	42	2e-04
GSP:W64144	W64144	Human Kunitz-type serine protease inhibitor d...	42	2e-04
GSP:Y52594	Y52594	Wild-type human Kunitz domain, zkun5.	42	2e-04
GSP:Y52597	Y52597	Human zkun5 protein (portion).	42	2e-04
GSP:R39792	R39792	Human Kunitz-type protease inhibitor.	42	3e-04

GSP:W18449	W18449	Alpha mating factor:KPI(-4-57;M15L,S17F) enco...	42	3e-04
GSP:W18418	W18418	KPI(-4 to 57) S17F. >GSP:Y68081 Y68081 Kunitz...	42	3e-04
GSP:Y68037	Y68037	Kunitz protease inhibitor analogue protein se...	42	3e-04
GSP:W18426	W18426	KPI(-4 to 57) M15A, S17F. >GSP:Y68042 Y68042 ...	41	4e-04
GSP:W19809	W19809	Alpha mating factor:KPI(-4-57;M15A,S17F) enco...	41	4e-04
GSP:W18551	W18551	Kunitz type active site inhibitor domain IV-4...	41	4e-04
GSP:Y68149	Y68149	Kunitz protease inhibitor variant BG006.	41	4e-04
GSP:Y68163	Y68163	Kunitz protease inhibitor variant DD116.	41	4e-04
GSP:W30052	W30052	Human placental bikunin.	41	5e-04
GSP:W64146	W64146	Human Kunitz-type serine protease inhibitor d...	41	5e-04
GSP:W64122	W64122	Human Kunitz-type serine protease inhibitor d...	41	5e-04
GSP:W64124	W64124	Human Kunitz-type serine protease inhibitor d...	41	5e-04
GSP:W64128	W64128	Human Kunitz-type serine protease inhibitor d...	41	5e-04
GSP:W64130	W64130	Human Kunitz-type serine protease inhibitor d...	41	5e-04
GSP:Y68100	Y68100	Kunitz protease inhibitor variant TW6140.	41	5e-04
GSP:Y68141	Y68141	Kunitz protease inhibitor variant TW6187.	41	5e-04
GSP:R22978	R22978	Aprotinin analogue #3 with reduced nephrotoxi...	41	7e-04
GSP:R22976	R22976	Aprotinin analogue #1 with reduced nephrotoxi...	41	7e-04
GSP:R22980	R22980	Aprotinin analogue #5 with reduced nephrotoxi...	41	7e-04
GSP:W18450	W18450	Alpha mating factor:KPI(-4-57;M15L,S17Y) enco...	41	7e-04
GSP:W18419	W18419	KPI(-4 to 57) S17Y. >GSP:Y68082 Y68082 Kunitz...	41	7e-04
GSP:W64148	W64148	Human Kunitz-type serine protease inhibitor d...	41	7e-04
GSP:W64125	W64125	Human Kunitz-type serine protease inhibitor d...	41	7e-04
GSP:W64127	W64127	Human Kunitz-type serine protease inhibitor d...	41	7e-04
GSP:Y68038	Y68038	Kunitz protease inhibitor analogue protein se...	41	7e-04
GSP:Y68164	Y68164	Kunitz protease inhibitor variant TW6191.	41	7e-04
STR:O95428	O95428	HYPOTHETICAL 133.5 KDA PROTEIN. >GNP:AF109907...	41	7e-04
GSP:R22977	R22977	Aprotinin analogue #2 with reduced nephrotoxi...	40	0.001
GSP:W18448	W18448	Alpha mating factor:KPI(-4-57;M15A,S17Y) enco...	40	0.001
GSP:W18427	W18427	KPI(-4 to 57) M15A, S17Y. >GSP:Y68036 Y68036 ...	40	0.001
GSP:W19808	W19808	phoA:KIP(1-55;M15A,S17F):geneIII fusion. >GSP...	40	0.001
GSP:W63684	W63684	Human secreted protein 4.	40	0.001
GSP:Y68062	Y68062	Kunitz protease inhibitor variant TW6167.	40	0.001
GSP:W18444	W18444	Alpha mating factor:KPI(1-57) encoded by plas...	40	0.001
GSP:W18420	W18420	KPI(-4 to 57) S17W. >GSP:Y68083 Y68083 Kunitz...	40	0.001
GSP:W18557	W18557	Novel fusion protein TFKD1.	40	0.001
GSP:Y68073	Y68073	Kunitz protease inhibitor variant TW6179.	40	0.001
GSP:Y68142	Y68142	Kunitz protease inhibitor variant TW6188.	40	0.001
GSP:Y68144	Y68144	Kunitz protease inhibitor variant TW6170.	40	0.001
GSP:Y52595	Y52595	Gly20Ala mutant human zkun5 Kunitz domain.	40	0.001
GSP:W18447	W18447	Alpha mating factor:KPI(-4-57;M15A,S17W) enco...	39	0.002
GSP:W18422	W18422	KPI(-4 to 57) S17L. >GSP:Y68084 Y68084 Kunitz...	39	0.002
GSP:W18428	W18428	KPI(-4 to 57) M15A, S17W. >GSP:Y68035 Y68035 ...	39	0.002
GSP:W18413	W18413	KPI(-4 to 57) I16F. >GSP:Y68077 Y68077 Kunitz...	39	0.002
GSP:W18414	W18414	KPI(-4 to 57) I16K. >GSP:Y68078 Y68078 Kunitz...	39	0.002
GSP:W18416	W18416	KPI(-4 to 57) S17I.	39	0.002
GSP:Y68069	Y68069	Kunitz protease inhibitor variant DD109.	39	0.002
GSP:Y68093	Y68093	Kunitz protease inhibitor variant TW6142.	39	0.002
GSP:Y68121	Y68121	Kunitz protease inhibitor variant DD129.	39	0.002
GSP:Y68126	Y68126	Kunitz protease inhibitor variant TW6169.	39	0.002
GSP:Y68150	Y68150	Kunitz protease inhibitor variant DD130.	39	0.002
GSP:Y68156	Y68156	Kunitz protease inhibitor variant DD122.	39	0.002
GSP:Y68161	Y68161	Kunitz protease inhibitor variant BG024.	39	0.002
GSP:Y68170	Y68170	Kunitz protease inhibitor variant BG040.	39	0.002
GSP:P94777	P94777	Plasmid pSVMT-APPI carrying novel amyloid pre...	39	0.002
GSP:R05167	R05167	Sequence of amyloid precursor protein (APP).	39	0.002
GSP:R08109	R08109	Protein sDOG deduced from insert of plasmid p...	39	0.002
GSP:R08110	R08110	Protein sDJ deduced from insert of plasmid pS...	39	0.002
GSP:W18396	W18396	KPI(-4 to 57) R40A. >GSP:Y68117 Y68117 Kunitz...	39	0.002
GSP:W18424	W18424	KPI(-4 to 57) S17H.	39	0.002
GSP:W18430	W18430	KPI(-4 to 57) M15G, S17Y. >GSP:Y68129 Y68129 ...	39	0.002
GSP:W18412	W18412	KPI(-4 to 57) I16A. >GSP:Y68076 Y68076 Kunitz...	39	0.002
GSP:Y68063	Y68063	Kunitz protease inhibitor variant BG031.	39	0.002
GSP:Y68064	Y68064	Kunitz protease inhibitor variant BG032.	39	0.002
GSP:Y68105	Y68105	Kunitz protease inhibitor variant TW6157.	39	0.002
GSP:Y68109	Y68109	Kunitz protease inhibitor variant DD101.	39	0.002
GSP:Y68139	Y68139	Kunitz protease inhibitor variant BG003.	39	0.002
GSP:Y68143	Y68143	Kunitz protease inhibitor variant TW6189.	39	0.002
GSP:Y68151	Y68151	Kunitz protease inhibitor variant DD131.	39	0.002
GSP:Y68166	Y68166	Kunitz protease inhibitor variant BG029.	39	0.002
GSP:Y68181	Y68181	Yeast mating-factor and KPI-P48 protein seque...	39	0.002
GSP:Y68182	Y68182	KPI-P48 protein sequence Fig 42.	39	0.002
GSP:Y68157	Y68157	Kunitz protease inhibitor variant BG015.	39	0.003
GSP:Y68167	Y68167	Kunitz protease inhibitor variant BG030.	39	0.003
PIR:A32761	A32761	hypothetical Alzheimer's disease amyloid beta...	39	0.003
STR:Q13764	Q13764	AMYLOID-BETA PROTEIN. >GNP:M34875 M34875_1 Hu...	39	0.003
RTR:CAA02049	CAA02049	APP PRECURSOR PROTEIN (FRAGMENT). >GNP:A3...	39	0.003

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GNP:X06981|X06981_1|Human mRNA fragment for amyloid beta-protei... 39 0.003
GNP:X06982|X06982_1|Human mRNA fragment for amyloid beta-protei... 39 0.003
GSP:W30063|W30063|EST R74593 protein. 34 0.090
GSP:W30049|W30049|Human placental bikunin. 33 0.12
GSP:W30050|W30050|Human placental bikunin. 33 0.12
SP:P52788 O00544|SPSY_HUMAN|SPERMINE SYNTHASE (EC 2.5.1.22) (SP... 27 8.9
PIR:S54160|S54160|spermine synthase (EC 2.5.1.22) - human >GNP:... 27 8.9
STR:Q9UQS1|Q9UQS1|SPERMIDINE AMINOPROPYLTRANSFERASE (FRAGMENT)... 27 8.9
RTR:BAA20005|BAA20005|5'OY11.1 PROTEIN (FRAGMENT). >GNP:D87009|... 27 8.9

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>GSP:Y35928|Y35928|Extended human secreted protein sequence, SEQ
ID NO. 177.

Length = 99

Score = 214 bits (539), Expect = 4e-56
Identities = 99/99 (100%), Positives = 99/99 (100%)

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Query: 1  MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN 60
          MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN
Sbjct: 1  MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN 60

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Query: 61  RTSKRCETVFVSGCNGNLNNFKLKIERYVACVAKYKPPR 99
          RTSKRCETVFVSGCNGNLNNFKLKIERYVACVAKYKPPR
Sbjct: 61  RTSKRCETVFVSGCNGNLNNFKLKIERYVACVAKYKPPR 99

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>GSP:Y36054|Y36054|Extended human secreted protein sequence, SEQ

ID NO. 439.

Length = 99

Score = 210 bits (529), Expect = 5e-55
Identities = 97/99 (97%), Positives = 97/99 (97%)

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Query: 1  MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN 60
          MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN
Sbjct: 1  MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN 60

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Query: 61  RTSKRCETVFVSGCNGNLNNFKLKIERYVACVAKYKPPR 99
          RTSKRCETVFVFS CNGNLNNFKLKIERYV CVAKYKPPR
Sbjct: 61  RTSKRCETVFVSSCNGNLNNFKLKIERYVXCVAKYKPPR 99

```

>GSP:Y12791|Y12791|Human 5' EST secreted protein SEQ ID NO:381.

Length = 80

Score = 170 bits (427), Expect = 5e-43
Identities = 78/79 (98%), Positives = 78/79 (98%)

```

Query: 1  MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN 60
          MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN
Sbjct: 1  MKSAKLGFLRRFFIFCSLNTLLLGAVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYN 60

```

```

Query: 61  RTSKRCETVFVSGCNGNLN 79
          RTSKRCETVFVFS CNGNLN
Sbjct: 61  RTSKRCETVFVSSCNGNLN 79

```

>GSP:R81936|R81936|Human ITI-K1 Kunitz domain derived protein

DKI-4.1.1.

Length = 58

Score = 57.0 bits (135), Expect = 8e-09
Identities = 26/54 (48%), Positives = 31/54 (57%)

```

Query: 38  KDPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIERYVAC 91
          +D C+L + G C H RYFYN TS CETF + GC GN NNF + E C
Sbjct: 2  EDSCQLGYDAGPCRGAHPRYFYNGTSMACETFSYGGCGGNGNNFVTEKECLQTC 55

```

```

>SP:P02760 P02759 P00977|AMBP_HUMAN|AMBP PROTEIN PRECURSOR
[CONTAINS: ALPHA-1-MICROGLOBULIN (PROTEIN
HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN
CHARGE); INTER-ALPHA-TRYPSIN INHIBITOR LIGHT CHAIN
(ITI-LC) (BIKUNIN) (HI-30)]. >PIR:S13433 S10778 A93642
A90074 A90225 A90686 PN0450 B39079 A61580 B25604 C34245
A25303 A53110 S03552 S28930 S43466 A53642 S55688 I52208
S59509 S66434 S68728 S02431

```

A03217|HCHU|alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - human >GNP:X54816|X54816_1|Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.); alpha1-microglobulin. >GNP:X04494|X04494_1|Human mRNA for alpha-1-microglobulin and HI-30; precursor polypeptide. >GNP:X04225|X04225_1|Human mRNA for protein HC (alpha-1-microglobulin). >GNP:M88249|M88249_1|Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exons 7-10.
Length = 352

Score = 53.9 bits (127), Expect = 7e-08
Identities = 25/54 (46%), Positives = 31/54 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
+D C+L + G C + RYFYN TS CETF + GC GN NNF + E C
Sbjct: 228 EDSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTC 281

Score = 28.6 bits (62), Expect = 3.0
Identities = 19/70 (27%), Positives = 27/70 (38%), Gaps = 3/70 (4%)

Query: 25 GVNKIAEKICGDL--KDPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNF 81
G N + EK C C L + G C + ++ +C F + GC GN N F
Sbjct: 268 GNNFVTEKECLQTCRTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNNGKF 327

Query: 82 KLKIEREVAC 91
+ E C
Sbjct: 328 YSEKECREYC 337

>GSP:R92237|R92237|Human wild-type urinary trypsin inhibitor.
>GSP:W25928|W25928|Anti-trypsin inhibitor UTI.
Length = 147

Score = 53.9 bits (127), Expect = 7e-08
Identities = 25/54 (46%), Positives = 31/54 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
+D C+L + G C + RYFYN TS CETF + GC GN NNF + E C
Sbjct: 23 EDSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTC 76

Score = 28.6 bits (62), Expect = 3.0
Identities = 19/70 (27%), Positives = 27/70 (38%), Gaps = 3/70 (4%)

Query: 25 GVNKIAEKICGDL--KDPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNF 81
G N + EK C C L + G C + ++ +C F + GC GN N F
Sbjct: 63 GNNFVTEKECLQTCRTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNNGKF 122

Query: 82 KLKIEREVAC 91
+ E C
Sbjct: 123 YSEKECREYC 132

>GSP:R78553|R78553|Human ITI Kunitz domain 1.
>GSP:W64115|W64115|Human Kunitz-type serine protease inhibitor domain #11. >GSP:W92862|W92862|US5880256 Seq ID 38.
Length = 58

Score = 53.9 bits (127), Expect = 7e-08
Identities = 25/54 (46%), Positives = 31/54 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
+D C+L + G C + RYFYN TS CETF + GC GN NNF + E C
Sbjct: 2 EDSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTC 55

>GSP:R99217|R99217|Inter alpha trypsin inhibitor (ITI) light chain.
Length = 55

Score = 53.9 bits (127), Expect = 7e-08
Identities = 25/54 (46%), Positives = 31/54 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNFKLKIIEVAC 91
 +D C+L + G C + RYFYN TS CETF + GC GN NNF + E C
 Sbjct: 2 EDSCQLGYSAGPCMGMTSRFYNGTSMACETFQYGGCMGNGNMFVTEKECLQTC 55

>GSP:P81110|P81110|Sequence of new fusion protein contg.
 alpha-1-microglobulin (AMG) and the HI-30 region of
 inter-alpha-trypsin inhibitor (III) light chain.
 Length = 352

Score = 53.9 bits (127), Expect = 7e-08
 Identities = 25/54 (46%), Positives = 31/54 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNFKLKIIEVAC 91
 +D C+L + G C + RYFYN TS CETF + GC GN NNF + E C
 Sbjct: 228 EDSCQLGYSAGPCMGMTSRFYNGTSMACETFQYGGCMGNGNMFVTEKECLQTC 281

Score = 28.6 bits (62), Expect = 3.0
 Identities = 19/70 (27%), Positives = 27/70 (38%), Gaps = 3/70 (4%)

Query: 25 GVNKIAEKICGDL---KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNFKLKIIEVAC 81
 G N + EK C C L + G C + ++ +C F + GC GN N F
 Sbjct: 268 GNNFVTEKECLQTCRTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQNGNKF 327

Query: 82 KLKIIEVAC 91
 + E C
 Sbjct: 328 YSEKECREYC 337

>STR:P78491|P78491|ALPHA-1-MICROGLOBULIN (FRAGMENT).
 >GNP:X54818|X54818_1|Human gene for
 alpha-1-microglobulin-bikunin, exons 7-10 (encoding
 linker peptide and bikunin); alpha-1-microglobulin.
 Length = 151

Score = 53.9 bits (127), Expect = 7e-08
 Identities = 25/54 (46%), Positives = 31/54 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNFKLKIIEVAC 91
 +D C+L + G C + RYFYN TS CETF + GC GN NNF + E C
 Sbjct: 27 EDSCQLGYSAGPCMGMTSRFYNGTSMACETFQYGGCMGNGNMFVTEKECLQTC 80

Score = 28.6 bits (62), Expect = 3.0
 Identities = 19/70 (27%), Positives = 27/70 (38%), Gaps = 3/70 (4%)

Query: 25 GVNKIAEKICGDL---KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNFKLKIIEVAC 81
 G N + EK C C L + G C + ++ +C F + GC GN N F
 Sbjct: 67 GNNFVTEKECLQTCRTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQNGNKF 126

Query: 82 KLKIIEVAC 91
 + E C
 Sbjct: 127 YSEKECREYC 136

>GSP:W69522|W69522|rUTI protein SEQ ID NO:24 from WO9829453 Claim
 14.
 Length = 147

Score = 53.9 bits (127), Expect = 7e-08
 Identities = 25/54 (46%), Positives = 31/54 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNFKLKIIEVAC 91
 +D C+L + G C + RYFYN TS CETF + GC GN NNF + E C
 Sbjct: 23 EDSCQLGYSAGPCMGMTSRFYNGTSMACETFQYGGCMGNGNMFVTEKECLQTC 76

Score = 27.8 bits (60), Expect = 5.2
 Identities = 19/70 (27%), Positives = 26/70 (37%), Gaps = 3/70 (4%)

Query: 25 GVNKIAEKICGDL---KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNFKLKIIEVAC 81
 G N + EK C C L + G C + ++ +C F + GC GN N F
 Sbjct: 63 GNNFVTEKECLQTCRTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQNGNKF 122

Query: 82 KLKIIEVAC 91
 + E C

Sbjct: 123 YSEKECREYC 132

>GSP:R99157|R99157|Human aprotinin-like Kunitz domain (ITI-D1).
Length = 58

Score = 53.5 bits (126), Expect = 9e-08
Identities = 23/44 (52%), Positives = 28/44 (63%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNF 81
+D C+L + G C + RYFYN TS CETF + GC GN NNF

Sbjct: 2 EDSCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNF 45

>GSP:R92233|R92233|Human mature urinary trypsin inhibitor with
modified kunitz domain 1.
Length = 124

Score = 53.1 bits (125), Expect = 1e-07
Identities = 25/54 (46%), Positives = 30/54 (55%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVAC 91
+D C+L + G C RYFYN TS CETF + GC GN NNF + E C

Sbjct: 2 EDSCQLGYSAGPCIAFFPRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTC 55

Score = 28.6 bits (62), Expect = 3.0
Identities = 19/70 (27%), Positives = 27/70 (38%), Gaps = 3/70 (4%)

Query: 25 GVNKIAEKICGDL---KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNF 81
G N + EK C C L + G C + ++ +C F + GC GN N F

Sbjct: 42 GNNFVTEKECLQTCRTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNKNF 101

Query: 82 KLKIEREVAC 91
+ E C

Sbjct: 102 YSEKECREYC 111

>GSP:R92235|R92235|Human urinary trypsin inhibitor with modified
kunitz domain 1.
Length = 145

Score = 53.1 bits (125), Expect = 1e-07
Identities = 25/54 (46%), Positives = 30/54 (55%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVAC 91
+D C+L + G C RYFYN TS CETF + GC GN NNF + E C

Sbjct: 23 EDSCQLGYSAGPCIAFFPRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTC 76

Score = 28.6 bits (62), Expect = 3.0
Identities = 19/70 (27%), Positives = 27/70 (38%), Gaps = 3/70 (4%)

Query: 25 GVNKIAEKICGDL---KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNF 81
G N + EK C C L + G C + ++ +C F + GC GN N F

Sbjct: 63 GNNFVTEKECLQTCRTVAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNKNF 122

Query: 82 KLKIEREVAC 91
+ E C

Sbjct: 123 YSEKECREYC 132

>GSP:R92238|R92238|Human UTI modified kunitz domain 1 and flanking
sequences.
Length = 74

Score = 53.1 bits (125), Expect = 1e-07
Identities = 25/54 (46%), Positives = 30/54 (55%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVAC 91
+D C+L + G C RYFYN TS CETF + GC GN NNF + E C

Sbjct: 5 EDSCQLGYSAGPCIAFFPRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTC 58

>GSP:W25929|W25929|Anti-trypsin inhibitor UTI Kunitz domain 1.
Length = 51

Score = 51.9 bits (122), Expect = 3e-07
Identities = 24/51 (47%), Positives = 29/51 (56%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
C+L + G C RYFYFN TS C+TFV+ GC GN NNF + E C
Sbjct: 1 CQLGYSAGPCIAFFPRYFYNGTSMACQTFVYGGCMGNNFVTEKECLQTC 51

>GSP:R81915|R81915|LACI Kunitz domain LACI-K2 derived protein
DKI-1.2.1.
Length = 58

Score = 51.5 bits (121), Expect = 4e-07
Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
D C L+ + G C H R+FYN +K+CE F + GC GN NNF+ E + C
Sbjct: 3 DFCLEEDGGRCRGAHPRWFYNNQTKQCEFSYGGCGNNNNFETLEECKNIC 55

>GSP:W61536|W61536|Human tissue factor pathway inhibitor-2
(TFPI-2).
Length = 213

Score = 51.5 bits (121), Expect = 4e-07
Identities = 23/70 (32%), Positives = 39/70 (54%)

Query: 30 AEKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREV 89
A++ G+ + C L +++G C + RY+Y+R ++ C F++ GC GN NNF +
Sbjct: 3 AQEPTGNNAEICLLPLDYGPCRALLRYYDYRTQSCRQFLYGGCEGNANNFYTWEACDD 62

Query: 90 ACVAKYKPPR 99
AC K P+
Sbjct: 63 ACWRIEKVPK 72

Score = 41.0 bits (94), Expect = 5e-04
Identities = 21/65 (32%), Positives = 31/65 (47%), Gaps = 2/65 (3%)

Query: 34 CGDLKDP--CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
C K P C + G C RY++N + C+ F ++GC GN NNF + + + AC
Sbjct: 127 CAPKKIPSFYCYSFKDEGLCSANVTRYFNPRTCDFTYTGCGGNDNNFVSREDCKRAC 186

Query: 92 VAKYK 96
K
Sbjct: 187 AKALK 191

Score = 29.0 bits (63), Expect = 2.3
Identities = 16/60 (26%), Positives = 27/60 (44%), Gaps = 3/60 (5%)

Query: 41 CKLDMNFGS-CYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPPR 99
C+L ++ C +YF+N +S CE F GC + N + + E C+ P +
Sbjct: 74 CRLQVSVDDQCEGSTEKYFFNLSSMTCEKFFSGGC--HRNRIENRFPDEATCMGFCAPKK 131

>SP:P48307|TFP2_HUMAN|TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR
(TFPI-2) (PLACENTALPROTEIN 5) (PP5).
>GSP:R74977|R74977|Human Kunitz-type protease-inhibitor
TFPI-2. >PIR:A54951 I55185 A34029 C34029
B34029|A54951|tissue factor pathway inhibitor-2
precursor - human >GNP:AC002076|AC002076_3|Human BAC
clone GS1-345D13 from 7q31-q32, complete sequence;
GS345D13.1; match to cDNA D29992 (NID:g484050); coded
for by human cDNA D29992 (NID:g484050).
>GNP:L27624|L27624_1|Homo sapiens tissue factor pathway
inhibitor-2 mRNA, complete cds; putative.
>GNP:D29992|D29992_1|Homo sapiens mRNA for placental
protein 5 (PP5), complete cds; putative.
Length = 235

Score = 51.5 bits (121), Expect = 4e-07
Identities = 23/70 (32%), Positives = 39/70 (54%)

Query: 30 AEKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREV 89
A++ G+ + C L +++G C + RY+Y+R ++ C F++ GC GN NNF +
Sbjct: 25 AQEPTGNNAEICLLPLDYGPCRALLRYYDYRTQSCRQFLYGGCEGNANNFYTWEACDD 84

Query: 90 ACVAKYKPPR 99
 AC K P+
 Sbjct: 85 ACWRIEKVPK 94

Score = 41.0 bits (94), Expect = 5e-04
 Identities = 21/65 (32%), Positives = 31/65 (47%), Gaps = 2/65 (3%)

Query: 34 CGDLKDP--CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C K P C + G C RY++N + C+ F ++GC GN NNF + + + AC
 Sbjct: 149 CAPKKIPSPFCYSPKDEGLCSANVTRYFNPRTCDFTYTGCGGNDNNFVSREDCKRAC 208

Query: 92 VAKYK 96
 K
 Sbjct: 209 AKALK 213

Score = 29.0 bits (63), Expect = 2.3
 Identities = 16/60 (26%), Positives = 27/60 (44%), Gaps = 3/60 (5%)

Query: 41 CKLDMNFGS-CYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPPR 99
 C+L ++ C +YF+N +S CE F GC + N + + E C+ P +
 Sbjct: 96 CRLQVSVDDQCEGSTKEYFFNLSSMTCEKFFSGGC--HRNRIENRFPDEATCMGFCAKK 153

>GSP:R42309|R42309|LAC1 gene product.
 Length = 304

Score = 51.2 bits (120), Expect = 5e-07
 Identities = 24/53 (45%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 D C L+ + G C RYFYNN SK+CE F + GC GN+NNF+ E + C
 Sbjct: 123 DFCFLEEDPGICRGYITRYFYNNQSKQCFKYGCGCLGNMNNFETLECKNTC 175

Score = 43.8 bits (101), Expect = 8e-05
 Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C + R+F+N +++CE F++ GC GN N F+ E + C
 Sbjct: 54 CAFKPDGPGCAIMKRFFFNIFTRQCEEFIYGGCGGNQNRFESEMECKKVC 104

Score = 41.8 bits (96), Expect = 3e-04
 Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C R++YN +C F +SGC GN NNF K E AC
 Sbjct: 217 CLAPADRGLCRANENRFYNSVIGKCRPFKYSGCGNENNFETSKRECLRAC 267

>GSP:R81921|R81921|Human TFPI-2 domain 3 Kunitz domain derived
 peptide DK1-3.1.1.
 Length = 58

Score = 51.2 bits (120), Expect = 5e-07
 Identities = 19/41 (46%), Positives = 26/41 (63%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNF 81
 C L ++ G C H RY+Y+R ++ CE F + GC GN NNF
 Sbjct: 5 CLLPLDGGPCRAAHLRYYYDRYTQSCEQFSYGGCEGNANNF 45

>GSP:R92231|R92231|Human urinary trypsin inhibitor modified kunitz
 domain 1.
 Length = 51

Score = 50.8 bits (119), Expect = 6e-07
 Identities = 24/51 (47%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C+L + G C RYFYNN TS CETF + GC GN NNF + E C
 Sbjct: 1 CQLGYSAGPCIAFFRYFYNGTSMACETFYGGCMGNGNMFVTEKECLQTC 51

>GSP:W00017|W00017|TFPI chimeric protein.
Length = 161

Score = 50.0 bits (117), Expect = 1e-06
Identities = 23/53 (43%), Positives = 32/53 (59%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNFKLKIIEVAC 91
D C L+ + G C RYFYN+ +K+CE F + GC GN+NNF+ E + C
Sbjct: 95 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 147

Score = 43.4 bits (100), Expect = 1e-04
Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNFKLKIIEVAC 91
C + G C + R+F+N +++CE F++ GC GN N F+ E + C
Sbjct: 26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 76

>GSP:R92265|R92265|TFPI mutein, Lys36Arg.
Length = 276

Score = 49.6 bits (116), Expect = 1e-06
Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNFKLKIIEVAC 91
D C L+ + G C RYFYN +K+CE F + GC GN+NNF+ E + C
Sbjct: 95 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 147

Score = 43.4 bits (100), Expect = 1e-04
Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNFKLKIIEVAC 91
C + G C + R+F+N +++CE F++ GC GN N F+ E + C
Sbjct: 26 CAFKADDGPCRAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 76

Score = 41.8 bits (96), Expect = 3e-04
Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNFKLKIIEVAC 91
C + G C R++YN +C F +SGC GN NNF K E AC
Sbjct: 189 CLTPADRGLCRANENRFYNSVIGKCRPFKYSGCGNENNFTSKQECLRAC 239

>GSP:R92011|R92011|Ubiquitin-TFPI fusion protein.
Length = 352

Score = 49.6 bits (116), Expect = 1e-06
Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNFKLKIIEVAC 91
D C L+ + G C RYFYN +K+CE F + GC GN+NNF+ E + C
Sbjct: 171 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 223

Score = 43.4 bits (100), Expect = 1e-04
Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNFKLKIIEVAC 91
C + G C + R+F+N +++CE F++ GC GN N F+ E + C
Sbjct: 102 CAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 152

Score = 41.8 bits (96), Expect = 3e-04
Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNFKLKIIEVAC 91
C + G C R++YN +C F +SGC GN NNF K E AC
Sbjct: 265 CLTPADRGLCRANENRFYNSVIGKCRPFKYSGCGNENNFTSKQECLRAC 315

>GSP:W47435|W47435|Aprotinin variant 4.
Length = 57

Score = 49.6 bits (116), Expect = 1e-06

Identities = 22/45 (48%), Positives = 26/45 (56%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFK 82
 +D C + G C RYFYNN T+ CETFV+ GC N NNFK
 Sbjct: 1 RDFCLEPPSTGPCRASIIRYFYNNATAGLCETFVYGGCRANRNNFK 45

>STR:O95103|O95103|TISSUE FACTOR PATHWAY INHIBITOR BETA.
 >GNP:AF021834|AF021834_1|Homo sapiens tissue factor
 pathway inhibitor beta (TFPIbeta) mRNA, complete cds;
 Kunitz-type protease inhibitor.
 Length = 251

Score = 49.6 bits (116), Expect = 1e-06
 Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
 D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
 Sbjct: 123 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 175

Score = 43.4 bits (100), Expect = 1e-04
 Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
 C + G C + R+F+N +++CE F++ GC GN N F+ E + C
 Sbjct: 54 CAFKADDGPCKAIMKRFFFNIFTRQCEEFYGGCEGNQNRFSLEECKKMC 104

>GSP:W30311|W30311|Recombinant non-glycosylated TFPI.
 >GSP:W61535|W61535|Human tissue factor pathway inhibitor
 (TFPI).
 Length = 276

Score = 49.6 bits (116), Expect = 1e-06
 Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
 D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
 Sbjct: 95 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 147

Score = 43.4 bits (100), Expect = 1e-04
 Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
 C + G C + R+F+N +++CE F++ GC GN N F+ E + C
 Sbjct: 26 CAFKADDGPCKAIMKRFFFNIFTRQCEEFYGGCEGNQNRFSLEECKKMC 76

Score = 41.8 bits (96), Expect = 3e-04
 Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
 C + G C R++YN +C F +SGC GN NNF K E AC
 Sbjct: 189 CLTPADRGLCRANENRFYNNVIGKCRPFKYSGCGNENNFSTKQECLRAC 239

>GSP:Y70273|Y70273|Human tissue factor pathway inhibitor protein
 (TFPI).
 Length = 304

Score = 49.6 bits (116), Expect = 1e-06
 Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
 D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
 Sbjct: 123 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 175

Score = 41.8 bits (96), Expect = 3e-04
 Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
 C + G C R++YN +C F +SGC GN NNF K E AC
 Sbjct: 217 CLTPADRGLCRANENRFYNNVIGKCRPFKYSGCGNENNFSTKQECLRAC 267

Score = 40.2 bits (92), Expect = 0.001
Identities = 16/51 (31%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIEREVAC 91
C + G C + R+F+N +++CE F++ GC N N F+ E + C
Sbjct: 54 CAFKADDGPCKAIMKRFFFNIFTRQCEEFYGGCEENQNRFSLEECKKMC 104

>GSP:R39802|R39802|TFPI 2.
>GSP:R81914|R81914|Lipoprotein-associated coagulation
inhibitor Kunitz domain LACI-K2.
>GSP:R99189|R99189|Human aprotinin-like Kunitz domain
(LACI-D2). >GSP:W64113|W64113|Human Kunitz-type serine
protease inhibitor domain #9.
>GSP:W92860|W92860|US5880256 Seq ID 36.
Length = 58

Score = 49.6 bits (116), Expect = 1e-06
Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIEREVAC 91
D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
Sbjct: 3 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 55

>GSP:Y70272|Y70272|Human mutant tissue factor pathway inhibitor
protein (TFPI).
Length = 304

Score = 49.6 bits (116), Expect = 1e-06
Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIEREVAC 91
D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
Sbjct: 123 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 175

Score = 41.8 bits (96), Expect = 3e-04
Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIEREVAC 91
C + G C R++YN +C F +SGC GN NNF K E AC
Sbjct: 217 CLTPADRGLCRANENRFYNNVIGKCRPFKYSGCGNENNFTSKQECLRAC 267

Score = 40.2 bits (92), Expect = 0.001
Identities = 16/51 (31%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIEREVAC 91
C + G C + R+F+N +++CE F++ GC N N F+ E + C
Sbjct: 54 CAFKADDGPCKAIMKRFFFNIFTRQCEEFYGGCEENQNRFSLEECKKMC 104

>RTR:CAA01311|CAA01311|KUNITZ-TYPE PROTEASE INHIBITOR.
>GNP:A17003|A17003_1|Kunitz-type protease inhibitor
domain 1 of TFPI seq ID No: 3.
Length = 255

Score = 49.6 bits (116), Expect = 1e-06
Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIEREVAC 91
D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
Sbjct: 74 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 126

Score = 43.4 bits (100), Expect = 1e-04
Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIEREVAC 91
C + G C + R+F+N +++CE F++ GC GN N F+ E + C
Sbjct: 5 CAFKADDGPCKAIMKRFFFNIFTRQCEEFYGGCEGNQNRFSLEECKKMC 55

Score = 41.8 bits (96), Expect = 3e-04
Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C R++YN +C F +SGC GN NNF K E AC
 Sbjct: 168 CLTPADRGLCRANENRFYNSVIGKCRPFKYSGCGNENNFSTKQECRLAC 218

>GSP:R23799|R23799|LACI fragment 90 - 160.
 Length = 71

Score = 49.6 bits (116), Expect = 1e-06
 Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
 Sbjct: 6 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 58

>SP:P10646|TFPI_HUMAN|TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR
 (TFPI) (LIPOPROTEIN-ASSOCIATED COAGULATION INHIBITOR)
 (LACI) (EXTRINSIC PATHWAY INHIBITOR) (EPI).
 >GSP:R81884|R81884|Lipoprotein-associated coagulation
 inhibitor (LACI). >GSP:R67994|R67994|Tissue factor
 pathway inhibitor. >GSP:Y49557|Y49557|Human lipoprotein
 associated coagulation inhibitor protein sequence.
 >PIR:A23712 A39176 A28650 A60433 B60433 S13034 A34315
 A38294 S03903|TIHUGK|tissue factor pathway inhibitor
 precursor - human >GNP:J03225|J03225_1|Human
 lipoprotein-associated coagulation inhibitor mRNA,
 complete cds; lipoprotein-associated coagulation
 inhibitor precursor. >GNP:M58650|M58650_1|Human
 lipoprotein associated coagulation inhibitor (LACI)
 gene, exon 9. >GNP:M59499|M59499_1|Human
 lipoprotein-associated coagulation inhibitor (LACI)
 gene, exon 9 and complete cds.
 Length = 304

Score = 49.6 bits (116), Expect = 1e-06
 Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
 Sbjct: 123 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 175

Score = 43.4 bits (100), Expect = 1e-04
 Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C + R+F+N +++CE F++ GC GN N F+ E + C
 Sbjct: 54 CAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 104

Score = 41.8 bits (96), Expect = 3e-04
 Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C R++YN +C F +SGC GN NNF K E AC
 Sbjct: 217 CLTPADRGLCRANENRFYNSVIGKCRPFKYSGCGNENNFSTKQECRLAC 267

>GSP:R23800|R23800|LACI fragment 1 - 160.
 Length = 160

Score = 49.6 bits (116), Expect = 1e-06
 Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
 Sbjct: 95 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 147

Score = 43.4 bits (100), Expect = 1e-04
 Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C + R+F+N +++CE F++ GC GN N F+ E + C
 Sbjct: 26 CAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 76

>GSP:P92002|P92002|Human tissue factor inhibitor (TFI).
Length = 304

Score = 49.6 bits (116), Expect = 1e-06
Identities = 23/53 (43%), Positives = 31/53 (58%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
D C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
Sbjct: 123 DFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 175

Score = 41.8 bits (96), Expect = 3e-04
Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
C + G C R++YN +C F +SGC GN NNF K E AC
Sbjct: 217 CLTPADRGLCRANENRFYNSVIGKCRPFKYSGCGNENNFSTKQECLRAC 267

Score = 41.0 bits (94), Expect = 5e-04
Identities = 16/51 (31%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
C + G C + R+F+N +++CE F++ C GN N F+ E + C
Sbjct: 54 CAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGACEGNQNRFSLEECKKMC 104

>GSP:R81933|R81933|Human HKI B9 domain Kunitz domain derived
protein DKI-6.1.
Length = 58

Score = 48.8 bits (114), Expect = 2e-06
Identities = 22/55 (40%), Positives = 28/55 (50%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
L + C M G C H R+F+N + CE F + GC GN NNF K + E C
Sbjct: 1 LPNVCAFPMEDGPCRAAHPRWFFNFETGECEEFAYGCGGNSNNFLRKEKCEKFC 55

>GSP:R81919|R81919|Human collagen alpha-3 Kunitz domain derived
protein DKI-2.1.
Length = 58

Score = 48.8 bits (114), Expect = 2e-06
Identities = 20/53 (37%), Positives = 29/53 (53%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
D CKL + G+C H +++Y+ +K C F + GC GN N F + E E C
Sbjct: 3 DICKLPKDEGTCAAHLKWWYDPNTKSCEFSYGGCGGNENKFGSQKECEKVC 55

>GSP:R92258|R92258|TFPI-2 first Kunitz-type domain.
Length = 51

Score = 48.8 bits (114), Expect = 2e-06
Identities = 17/41 (41%), Positives = 27/41 (65%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNF 81
C L +++G C + RY+Y+R ++ C F++ GC GN NNF
Sbjct: 1 CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNF 41

>GSP:R92259|R92259|TFPI second Kunitz-type domain.
Length = 51

Score = 48.8 bits (114), Expect = 2e-06
Identities = 22/51 (43%), Positives = 30/51 (58%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVVFSGCNGNLNNFKLKIEREVAC 91
C L+ + G C RYFYNN +K+CE F + GC GN+NNF+ E + C
Sbjct: 1 CFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNIC 51

>GSP:R74976|R74976|Generic human Kunitz-type protease-inhibitor.
Length = 53

Score = 48.8 bits (114), Expect = 2e-06
Identities = 17/41 (41%), Positives = 27/41 (65%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNF 81
C L +++G C + RY+Y+R ++ C F++ GC GN NNF
Sbjct: 3 CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNF 43

>GSP:R78547|R78547|Human TFPI-2 domain 1 Kunitz domain.
>GSP:R81920|R81920|Human TFPI-2 domain 1 Kunitz domain.
>GSP:R99173|R99173|Human aprotinin-like Kunitz domain
(TFPI2-D1).
Length = 58

Score = 48.8 bits (114), Expect = 2e-06
Identities = 17/41 (41%), Positives = 27/41 (65%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNF 81
C L +++G C + RY+Y+R ++ C F++ GC GN NNF
Sbjct: 5 CLLPLDYGPCRALLLRYYYDRYTQSCRQFLYGGCEGNANNF 45

>GSP:R81899|R81899|Kallikrein inhibitor protein KKI/3(b).
Length = 58

Score = 48.4 bits (113), Expect = 3e-06
Identities = 18/51 (35%), Positives = 29/51 (56%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIIEVAC 91
C + G C +H R+F+N +++CE F++ GC GN N F+ E + C
Sbjct: 5 CAFKADDGPCKAIHLRFFFNIFTRQCEEFYGGCEGNQNRFESELECKKMC 55

>GSP:W47432|W47432|Aprotinin variant 1.
Length = 57

Score = 48.4 bits (113), Expect = 3e-06
Identities = 21/45 (46%), Positives = 26/45 (57%)

Query: 38 KDPCCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFK 82
+D C + G C RYFY+ T+ CETFV+ GC N NNFK
Sbjct: 1 RDFCLEPPSTGPCRAAIIRYFYDATAGLCETFVYGGCRANRNNFK 45

>GSP:Y70010|Y70010|Human Protease and associated protein-4 (PPRG-4).
Length = 164

Score = 48.0 bits (112), Expect = 4e-06
Identities = 24/67 (35%), Positives = 32/67 (46%), Gaps = 1/67 (1%)

Query: 32 KICGDLK-DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIIEVA 90
K C DLK D C++ G C ++Y++ C FV+ GC GN NNF+ K
Sbjct: 98 KKCLDLKQDVCEMPKETGPCLAYFLHWWYDKKDNCTCSMFVYGGCQGNNNNFQSKANCLNT 157

Query: 91 CVAKYKP 97
C K P
Sbjct: 158 CKNKRFP 164

>GSP:R78389|R78389|Human lipoprotein-associated coagulation
inhibitor.
Length = 304

Score = 48.0 bits (112), Expect = 4e-06
Identities = 23/53 (43%), Positives = 30/53 (56%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIIEVAC 91
D C L+ + G C RYFYN +K CE F + GC GN+NNF+ E + C
Sbjct: 123 DFCFLEEDPGICRGYITRYFYNNGTGKCERFKYGGCLGNMNNFETLEECKNIC 175

Score = 43.4 bits (100), Expect = 1e-04
Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFGSGCNGNLNNFKLKIIEVAC 91
C + G C + R+F+N +++CE F++ GC GN N F+ E + C

Sbjct: 54 CAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 104

Score = 41.8 bits (96), Expect = 3e-04
Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVAC 91
C + G C R++YN +C F +SGC GN NNF K E AC

Sbjct: 217 CLTPADRGLCRANENRFYNSVIGKCRPFKYSGCGNENNFTSKQECLRAC 267

>GSP:R81917|R81917|LACI Kunitz domain LACI-K3 derived protein
DKI-1.3.1.
Length = 58

Score = 48.0 bits (112), Expect = 4e-06
Identities = 22/51 (43%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVAC 91
C + G C H R++YN +CE F +SGC GN NNF K E AC

Sbjct: 5 CLTPADDGPCRAAHPRFYNSVIGKCEPFSYSGCGNENNFTSKQECLRAC 55

>STR:AAG00547|AAG00547|Eppin-2. >GNP:AF286369|AF286369_1|Homo
sapiens eppin-2 (EPPIN2) mRNA, complete cds.
Length = 117

Score = 48.0 bits (112), Expect = 4e-06
Identities = 24/67 (35%), Positives = 32/67 (46%), Gaps = 1/67 (1%)

Query: 32 KICGDLK-DPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVA 90
K C DLK D C++ G C ++Y++ C FV+ GC GN NNF+ K

Sbjct: 51 KKCLDLKQDVCEMPKETGPCLAYFLHWWYDKKDNTCSMFVYGGCQGNNNNFQSKANCLNT 110

Query: 91 CVAKYKP 97
C K P

Sbjct: 111 CKNKRFP 117

>GSP:W75219|W75219|Human secreted protein encoded by gene 24 clone
HTEBY11. >STR:AAG00546|AAG00546|Eppin-1.
>STR:AAG00548|AAG00548|Eppin-3.
>STR:O95925|O95925|DJ461P17.2 (PUTATIVE NOVEL PROTEIN
WITH A WAP-TYPE (WHEY ACIDICPROTEIN) 'FOUR-DISULFIDE
CORE' AND A KUNITZ/BOVINE PANCREATIC TRYPSININHIBITOR
DOMAIN). >GNP:AL118493|AL118493_1|Novel human gene
mapping to chromosome 20. >GNP:AF286368|AF286368_1|Homo
sapiens eppin-1 (EPPIN1) mRNA, complete cds.
>GNP:AF286370|AF286370_1|Homo sapiens eppin-3 (EPPIN3)
mRNA, complete cds.
Length = 133

Score = 48.0 bits (112), Expect = 4e-06
Identities = 24/67 (35%), Positives = 32/67 (46%), Gaps = 1/67 (1%)

Query: 32 KICGDLK-DPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVA 90
K C DLK D C++ G C ++Y++ C FV+ GC GN NNF+ K

Sbjct: 67 KKCLDLKQDVCEMPKETGPCLAYFLHWWYDKKDNTCSMFVYGGCQGNNNNFQSKANCLNT 126

Query: 91 CVAKYKP 97
C K P

Sbjct: 127 CKNKRFP 133

>GSP:R22979|R22979|Aprotinin analogue #4 with reduced
nephrotoxicity.
Length = 111

Score = 47.6 bits (111), Expect = 5e-06
Identities = 23/54 (42%), Positives = 30/54 (54%)

Query: 29 IA EKICGDLKDPCCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFK 82
+AE++ D C + G C RYFY+ T+ CETFV+ GC N NNFK

Sbjct: 46 MAERLEKRRPDFCLEPPSTGPCKARIIRYFYDATAGLCETFVYGGCRANRNNFK 99

>GSP:R39673|R39673|C-terminal Kunitz-type protease inhibitor

variant.
Length = 58

Score = 47.6 bits (111), Expect = 5e-06
Identities = 20/53 (37%), Positives = 30/53 (55%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
D CKL + G+C + +++Y+ +K C FV+ GC GN N F + E E C
Sbjct: 3 DICKLPKDTGTCLGLIIKWYYDPNTKSCARFVYGGCRGNENKFGSQKECEKVC 55

>GSP:R22985|R22985|Aprotinin analogue #10 with reduced
nephrotoxicity.
Length = 109

Score = 47.6 bits (111), Expect = 5e-06
Identities = 23/54 (42%), Positives = 32/54 (58%), Gaps = 2/54 (3%)

Query: 29 IA EKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
+AE++ + +D C + G C RYFY+ + C+TFV+ GC GN NNFK
Sbjct: 46 MAERL--EK RDFCLEPPSTGPCKARIIRYFYNAKAGLCQTFVYGGCRGNNGNNFK 97

>GSP:W47434|W47434|Aprotinin variant 3.
Length = 57

Score = 47.6 bits (111), Expect = 5e-06
Identities = 21/45 (46%), Positives = 26/45 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
+D C + G C RYFY+ T+ CETFV+ GC N NNFK
Sbjct: 1 RDFCLEPPSTGPCRASIIRYFYDATAGLCETFVYGGCRANRNNFK 45

>GSP:R22983|R22983|Aprotinin analogue #8 with reduced
nephrotoxicity.
Length = 109

Score = 47.6 bits (111), Expect = 5e-06
Identities = 23/54 (42%), Positives = 32/54 (58%), Gaps = 2/54 (3%)

Query: 29 IA EKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
+AE++ + +D C + G C RYFY+ T+ CETFV+ GC N NNFK
Sbjct: 46 MAERL--EK RDFCLEPPSTGPCKARIIRYFYDATAGLCETFVYGGCRANRNNFK 97

>GSP:W47433|W47433|Aprotinin variant 2.
Length = 57

Score = 47.3 bits (110), Expect = 7e-06
Identities = 21/45 (46%), Positives = 26/45 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
+D C + G C RYFY+ T+ CETFV+ GC N NNFK
Sbjct: 1 RDFCLEPPSTGPCRARIIRYFYDATAGLCETFVYGGCRANRNNFK 45

>GSP:R39677|R39677|C-terminal Kunitz-type protease inhibitor
variant.
Length = 56

Score = 46.9 bits (109), Expect = 9e-06
Identities = 20/53 (37%), Positives = 29/53 (53%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
D CKL + G+C + +++Y+ +K C FV+ GC GN N F + E E C
Sbjct: 1 DICKLPKDTGTCKGAILKWYYDPNTKSCARFVYGGCRGNENKFGSQKECEKVC 53

>GSP:R81898|R81898|Kallikrein inhibitor protein KKI/3(a).
Length = 58

Score = 46.9 bits (109), Expect = 9e-06
Identities = 18/51 (35%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
C + G C H R+F+N +++CE F++ GC GN N F+ E + C

Sbjct: 5 CAFKADDGRCKGAHLRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 55

>GSP:R81907|R81907|Kallikrein inhibitor protein KK2/#6.
Length = 58

Score = 46.9 bits (109), Expect = 9e-06
Identities = 19/51 (37%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
C + GSC H R+F+N +++CE F + GC GN N F+ E + C
Sbjct: 5 CAFKADDGSCRAAHLRWFFNIFTRQCEEFYGGCGGNQNRFSLEECKKMC 55

>GSP:R81897|R81897|Kallikrein inhibitor protein KKII/3#10.
Length = 58

Score = 46.9 bits (109), Expect = 9e-06
Identities = 18/51 (35%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
C + G C H R+F+N +++CE F++ GC GN N F+ E + C
Sbjct: 5 CAFKADDGHCKGAHLRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 55

>GSP:R39672|R39672|C-terminal Kunitz-type protease inhibitor
variant.
Length = 58

Score = 46.5 bits (108), Expect = 1e-05
Identities = 20/53 (37%), Positives = 28/53 (52%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
D CKL + G C + R++Y+ +K C F + GC N N FK + E E C
Sbjct: 3 DICKLPKDEGPCLDAILRWYYDPNTKSCARFWYGGCGANENKFKSQKECEKVC 55

>GSP:W47436|W47436|Aprotinin variant 5.
Length = 57

Score = 46.5 bits (108), Expect = 1e-05
Identities = 20/45 (44%), Positives = 26/45 (57%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFK 82
+D C + G C RYFY+ T+ C+TFV+ GC N NNFK
Sbjct: 1 RDFCLEPPSTGPCRASIIRYFYDATAGLCQTFVYGGCRANRNNFK 45

>GSP:Y68039|Y68039|Kunitz protease inhibitor analogue protein
sequence Fig 31. >GSP:Y68136|Y68136|Kunitz protease
inhibitor variant TW6183.
Length = 61

Score = 46.1 bits (107), Expect = 2e-05
Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C +HFR++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMHFRWYFDVTEGKCAPFFYGGCGNRNNF----DTEECMA 55

>GSP:Y68148|Y68148|Kunitz protease inhibitor variant TW177.
Length = 61

Score = 46.1 bits (107), Expect = 2e-05
Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C +HFR++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRALHFRWYFDVTEGKCAPFFYGGCGNRNNF----DTEECMA 55

>GSP:R39676|R39676|C-terminal Kunitz-type protease inhibitor
variant.
Length = 56

Score = 46.1 bits (107), Expect = 2e-05

Identities = 20/53 (37%), Positives = 28/53 (52%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 D CKL + G C + R++Y+ +K C F + GC N N FK + E E C
 Sbjct: 1 DICKLPKDEGPCVDFILRWYYDPNTKSCARFWYGGCGANENKFKSQKECEKVC 53

>GSP:W19801|W19801|Alpha mating factor:KPI(-4-57;I16H,S17F) encoded
 by pTW6183. >GSP:Y68030|Y68030|Yeast
 mating-factor-KPI(-4-57) fusion protein sequence Fig 15.
 Length = 146

Score = 46.1 bits (107), Expect = 2e-05
 Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C +HFR++++ T +C F + GC GN NNF + E C+A
 Sbjct: 88 VREVCSEAETGPCRAMHFRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 140

>SP:P49223|KIB9_HUMAN|KUNITZ-TYPE PROTEASE INHIBITOR HKIB9
 (FRAGMENT). >PIR:S41399|S41399|Kunitz-type proteinase
 inhibitor HKIB9 - human >GNP:X77166|X77166_1|H.sapiens
 gene for kunitz-type protease inhibitor, HKIB9.
 Length = 64

Score = 45.7 bits (106), Expect = 2e-05
 Identities = 21/55 (38%), Positives = 27/55 (48%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 L + C M G C R+F+N + CE F + GC GN NNF K + E C
 Sbjct: 7 LPNVCAFPMEKGPCQTYMTRWFFNFETGECELFAYGGCGNSNFLRKEKCEKFC 61

>GSP:R22984|R22984|Aprotinin analogue #9 with reduced
 nephrotoxicity.
 Length = 141

Score = 45.7 bits (106), Expect = 2e-05
 Identities = 22/52 (42%), Positives = 27/52 (51%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
 E + D +D C G C RYFY+ T+ CETFV+ GC NNFK
 Sbjct: 78 EGVSLDKRDFCLEPPYTGPCKARIIRYFYDATAGLCETFVYGGCRAKRNNNFK 129

>GSP:R39678|R39678|C-terminal Kunitz-type protease inhibitor
 variant.
 Length = 56

Score = 45.7 bits (106), Expect = 2e-05
 Identities = 19/53 (35%), Positives = 29/53 (53%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 D CKL + G+C + +++Y+ +K C FV+ GC N FK + E E C
 Sbjct: 1 DICKLPKDEGTCLALIIKWYYDPNTKSCARFVYGGCRAKENKFKSQKECEKVC 53

>GSP:W30060|W30060|Human consensus bikunin.
 Length = 235

Score = 45.7 bits (106), Expect = 2e-05
 Identities = 26/69 (37%), Positives = 36/69 (51%), Gaps = 2/69 (2%)

Query: 18 LNTLLLGGVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGN 77
 L +LLL GV +A + D C + G C R++YN T C+ FV+ GC+GN
 Sbjct: 8 LGSLLLSGV--LAADRERSIHDFCLVSKVVGRCRASMPrWWYNVTDGSCQLFVYGGCDGN 65

Query: 78 LNNFKLKIE 86
 NN+ K E
 Sbjct: 66 SNNYLTKEE 74

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPP 98

C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 124 CTANAVTGPCRASFPWWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 181

>GSP:W30045|W30045|Human placental bikunin.
 Length = 240

Score = 45.7 bits (106), Expect = 2e-05
 Identities = 26/69 (37%), Positives = 36/69 (51%), Gaps = 2/69 (2%)

Query: 18 LNTLLLGGVNKKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVFGCNGN 77
 L +LLL GV +A + D C + G C R++YN T C+ FV+ GC+GN

Sbjct: 17 LGSLLLSGV--LAADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGN 74

Query: 78 LNNFKLKIE 86
 NN+ K E

Sbjct: 75 SNNYLTKEE 83

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVFGCNGNLNNFKLKIEREVACVAKYKPP 98

C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 133 CTANAVTGPCRASFPWWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 190

>GSP:W30043|W30043|Human placental bikunin.
 Length = 197

Score = 45.7 bits (106), Expect = 2e-05
 Identities = 26/69 (37%), Positives = 36/69 (51%), Gaps = 2/69 (2%)

Query: 18 LNTLLLGGVNKKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVFGCNGN 77
 L +LLL GV +A + D C + G C R++YN T C+ FV+ GC+GN

Sbjct: 8 LGSLLLSGV--LAADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGN 65

Query: 78 LNNFKLKIE 86
 NN+ K E

Sbjct: 66 SNNYLTKEE 74

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVFGCNGNLNNFKLKIEREVACVAKYKPP 98

C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 124 CTANAVTGPCRASFPWWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 181

>GSP:W30040|W30040|Human placental bikunin.
 >GSP:W13665|W13665|Hepatocyte growth factor activator
 inhibitor HAI-II. >GSP:W70286|W70286|Human tissue
 factor pathway inhibitor-3 (TFPI-3).
 >STR:000271|000271|BIKUNIN. >GNP:U78095|U78095_1|Homo
 sapiens placental bikunin mRNA, complete cds; member of
 the Kunitz family of protease inhibitors.
 Length = 252

Score = 45.7 bits (106), Expect = 2e-05
 Identities = 26/69 (37%), Positives = 36/69 (51%), Gaps = 2/69 (2%)

Query: 18 LNTLLLGGVNKKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVFGCNGN 77
 L +LLL GV +A + D C + G C R++YN T C+ FV+ GC+GN

Sbjct: 17 LGSLLLSGV--LAADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGN 74

Query: 78 LNNFKLKIE 86
 NN+ K E

Sbjct: 75 SNNYLTKEE 83

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVFGCNGNLNNFKLKIEREVACVAKYKPP 98

C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 133 CTANAVTGPCRASFPWWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 190

>STR:O43291|O43291|HEPATOCYTE GROWTH FACTOR ACTIVATOR INHIBITOR
TYPE 2. >GNP:AB006534|AB006534_1|Homo sapiens mRNA for
hepatocyte growth factor activator inhibitor type 2,
complete cds.
Length = 252

Score = 45.7 bits (106), Expect = 2e-05
Identities = 26/69 (37%), Positives = 36/69 (51%), Gaps = 2/69 (2%)

Query: 18 LNTLLLGGVNKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNRTSKRCETFVFGSGCNGN 77
L +LLL GV +A + D C + G C R++YN T C+ FV+ GC+GN
Sbjct: 17 LGSLLLSGV--LAADRERSIHDFCLVSKVVGRCRASMPRWWYNVTDGSCQLFVYGGCDGN 74

Query: 78 LNNFKLKIE 86
NN+ K E
Sbjct: 75 SNNYLTKEE 83

Score = 33.6 bits (75), Expect = 0.090
Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYNRTSKRCETFVFGSGCNGNLNNFKLKIEREVACVAKYKPP 98
C + G C R++++ C F++ GC GN N+++ + C + + P
Sbjct: 133 CTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 190

>GSP:R81932|R81932|Human HKI B9 domain Kunitz domain.
>GSP:R99208|R99208|Human aprotinin-like Kunitz domain
(HKI B9). >GSP:W64118|W64118|Human Kunitz-type serine
protease inhibitor domain #14.
>GSP:W92865|W92865|US5880256 Seq ID 41.
Length = 58

Score = 45.7 bits (106), Expect = 2e-05
Identities = 21/55 (38%), Positives = 27/55 (48%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRTSKRCETFVFGSGCNGNLNNFKLKIEREVAC 91
L + C M G C R+F+N + CE F + GC GN NNF K + E C
Sbjct: 1 LPNVCAFPMEKGPCQTYMTRWFFNFETGECELFAYGGCGGNSNNFLRKEKCEKFC 55

>STR:Q9UJG4|Q9UJG4|DJ461P17.8 (HKIB7 (KUNITZ/BOVINE PANCREATIC
TRYPSIN INHIBITOR DOMAINPROTEIN)) (FRAGMENT).
Length = 63

Score = 45.7 bits (106), Expect = 2e-05
Identities = 21/55 (38%), Positives = 27/55 (48%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRTSKRCETFVFGSGCNGNLNNFKLKIEREVAC 91
L + C M G C R+F+N + CE F + GC GN NNF K + E C
Sbjct: 6 LPNVCAFPMEKGPCQTYMTRWFFNFETGECELFAYGGCGGNSNNFLRKEKCEKFC 60

>RTR:CAA01298|CAA01298|KUNITZ TYPE PROTEASE INHIBITOR.
>RTR:E974000|E974000|KUNITZ-TYPE PROTEASE INHIBITOR SEQ
ID NO 1. >RTR:E974003|E974003|KUNITZ-TYPE PROTEASE
INHIBITOR SEQ ID NO 5. >GNP:A16758|A16758_1|Kunitz-type
protease inhibitor seq ID No 4; Protein sequence is in
conflict with the conceptual translation.
Length = 60

Score = 45.7 bits (106), Expect = 2e-05
Identities = 21/55 (38%), Positives = 27/55 (48%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRTSKRCETFVFGSGCNGNLNNFKLKIEREVAC 91
L + C M G C R+F+N + CE F + GC GN NNF K + E C
Sbjct: 3 LPNVCAFPMEKGPCQTYMTRWFFNFETGECELFAYGGCGGNSNNFLRKEKCEKFC 57

>GSP:W30044|W30044|Human consensus bikunin.
Length = 248

Score = 45.7 bits (106), Expect = 2e-05
Identities = 26/69 (37%), Positives = 36/69 (51%), Gaps = 2/69 (2%)

Query: 18 LNTLLLGGVNKAIEKICGDLKDPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGN 77
 L +LLL GV +A + D C + G C R++YN T C+ FV+ GC+GN
 Sbjct: 13 LGSLLLSGV--LAADRERSIHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGN 70

Query: 78 LNNFKLKIE 86
 NN+ K E
 Sbjct: 71 SNNYLTKEE 79

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPP 98
 C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 129 CTANAVTGPCRAAFPRWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 186

>GSP:Y68147|Y68147|Kunitz protease inhibitor variant TW176.
 Length = 61

Score = 45.7 bits (106), Expect = 2e-05
 Identities = 19/57 (33%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C HFR++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAAHFRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>SP:P12111 Q16501|CA36_HUMAN|COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR.
 >PIR:A59140 S13679 S24465 A57083 S28776 S00245 C31952
 C29848 S26510 S48709|CGHU3A|collagen alpha 3(VI) chain
 precursor [validated] - human
 >GNP:X52022|X52022_1|H.sapiens RNA for type VI collagen
 alpha3 chain.
 Length = 3176

Score = 45.3 bits (105), Expect = 3e-05
 Identities = 20/60 (33%), Positives = 30/60 (49%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPP 98
 D CKL + G+C + +++Y+ +K C F + GC GN N F + E E C P
 Sbjct: 3109 DICKLPKDEGTCRDFILKWYYPNTKSCARFWYGGCGGNENKFGSQKECEKVCAPVLAKP 3168

>GSP:R47542|R47542|Sequence of the last 70 AAs of the C5 domain of
 the type VI collagen alpha-3-chain (AAs 2873-2943)
 contg. the Kunitz type inhibitor domain.
 Length = 70

Score = 45.3 bits (105), Expect = 3e-05
 Identities = 20/60 (33%), Positives = 30/60 (49%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPP 98
 D CKL + G+C + +++Y+ +K C F + GC GN N F + E E C P
 Sbjct: 3 DICKLPKDEGTCRDFILKWYYPNTKSCARFWYGGCGGNENKFGSQKECEKVCAPVLAKP 62

>GSP:R81908|R81908|Kallikrein inhibitor protein KK2/#10.
 Length = 58

Score = 45.3 bits (105), Expect = 3e-05
 Identities = 19/51 (37%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C GSC H R+F+N +++CE F + GC GN N F+ E + C
 Sbjct: 5 CAFKAEGGSCRAAHQRWFFNIFTRQCEEFSGGCGGNQNRFSLEECKKMC 55

>SP:Q02388|CA17_HUMAN|COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR
 (LONG-CHAIN COLLAGEN) (LCCOLLAGEN).
 >GNP:L02870|L02870_1|Human alpha-1 type VII collagen
 (COL7A1) mRNA, complete cds.
 Length = 2944

Score = 44.9 bits (104), Expect = 4e-05
 Identities = 23/67 (34%), Positives = 33/67 (48%), Gaps = 8/67 (11%)

Query: 36 DLKDPCKLDMNFGSCYEVHFRYFYFYNR---TSKRCETFFVSGCNGNLNNFKLKIERYVACV 92
 D DPC L ++ GSC R+++ +++ C FV+ GC GN N F + E C
 Sbjct: 2871 DSDDPCSLPLDEGSCTAYTLRWYHRAVTGSTEACHPFVYGGCGGNANRFGTREACERRC- 2929

Query: 93 AKYKPPR 99
 PPR
 Sbjct: 2930 ----PPR 2932

>GSP:R78545|R78545|Human collagen alpha-3 Kunitz domain.
 >GSP:R81918|R81918|Human collagen alpha-3 Kunitz
 domain. >GSP:R99204|R99204|Human aprotinin-like Kunitz
 domain (A3 collagen). >GSP:W64117|W64117|Human
 Kunitz-type serine protease inhibitor domain #13.
 >GSP:W92864|W92864|US5880256 Seq ID 40.
 Length = 58

Score = 44.9 bits (104), Expect = 4e-05
 Identities = 19/53 (35%), Positives = 29/53 (53%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVAC 91
 D CKL + G+C + +++Y+ +K C F + GC GN N F + E E C
 Sbjct: 3 DICKLPKDEGTCDRFDILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVC 55

>GSP:R81926|R81926|Human TFPI-2 domain 3 Kunitz domain derived
 protein DK1-3.3.1. >GSP:R81935|R81935|Human ITI-K1
 Kunitz domain.
 Length = 58

Score = 44.9 bits (104), Expect = 4e-05
 Identities = 18/51 (35%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVAC 91
 C + G C H RY++N + C+ F ++GC GN NNF + + + AC
 Sbjct: 5 CYSPKDEGHCRAAHQRYFYFNPRYRTCDFTYTGCGGNDNNFVSREDCKRAC 55

>GSP:R81909|R81909|Kallikrein inhibitor protein KK2/#8.
 Length = 58

Score = 44.9 bits (104), Expect = 4e-05
 Identities = 18/51 (35%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVAC 91
 C + G C H R+F+N +++CE F + GC GN N F+ E + C
 Sbjct: 5 CAFKADDGPCRGAHLRFFFNIFTRQCEEFYGGCGGNQNRFESELECKKMC 55

>GSP:W19802|W19802|Alpha mating factor:KPI(-4-57;I16H,S17Y) encoded
 by pTW6184. >GSP:Y68031|Y68031|Yeast
 mating-factor-KPI(-4-57) fusion protein sequence Fig 16.
 Length = 146

Score = 44.9 bits (104), Expect = 4e-05
 Identities = 18/57 (31%), Positives = 31/57 (53%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVACVA 93
 +++ C G C +H+R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 88 VREVCSEQAETGPCRAMHYRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 140

>GSP:Y68040|Y68040|Kunitz protease inhibitor analogue protein
 sequence Fig 32. >GSP:Y68137|Y68137|Kunitz protease
 inhibitor variant TW6184.
 Length = 61

Score = 44.9 bits (104), Expect = 4e-05
 Identities = 18/57 (31%), Positives = 31/57 (53%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIERYVACVA 93
 +++ C G C +H+R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMHYRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>STR:Q14054|Q14054|COLLAGEN TYPE VII PRECURSOR.
 >GNP:L23982|L23982_1|Homo sapiens (clones: CW52-2,

CW27-6, CW15-2, CW26-5, 11-67) collagen type VII
intergenic region and (COL7A1) gene, complete cds.
Length = 2912

Score = 44.9 bits (104), Expect = 4e-05
Identities = 23/67 (34%), Positives = 33/67 (48%), Gaps = 8/67 (11%)

Query: 36 DLKDPCKLDMNFGSCYEVHFRYFYNR---TSKRCETVFVSGCNGNLNNFKLKIEREVACV 92
D DPC L ++ GSC R+++ +++ C FV+ GC GN N F + E C
Sbjct: 2839 DSDDPCSLPLDEGSCTAYTLRWYHRAVTGSTACHPFVYGGCGGNANRFGTREACERRC- 2897

Query: 93 AKYKPPR 99
PPR
Sbjct: 2898 ----PPR 2900

>GNP:L06862|L06862_1|Human type VII collagen (COL7A1) mRNA, 3' end;
base pairs 1-1167: triple-helix encoding region; base
pairs 1168-1653: non-collagenous NC-2 domain encoding
region.
Length = 550

Score = 44.9 bits (104), Expect = 4e-05
Identities = 23/67 (34%), Positives = 33/67 (48%), Gaps = 8/67 (11%)

Query: 36 DLKDPCKLDMNFGSCYEVHFRYFYNR---TSKRCETVFVSGCNGNLNNFKLKIEREVACV 92
D DPC L ++ GSC R+++ +++ C FV+ GC GN N F + E C
Sbjct: 477 DSDDPCSLPLDEGSCTAYTLRWYHRAVTGSTACHPFVYGGCGGNANRFGTREACERRC- 535

Query: 93 AKYKPPR 99
PPR
Sbjct: 536 ----PPR 538

>SP:Q06481|APP2_HUMAN|AMYLOID-LIKE PROTEIN 2 PRECURSOR (AMYLOID
PROTEIN HOMOLOG) (APPH) (CDEI-BOX BINDING PROTEIN)
(CDEBP). >PIR:A49321 S34644 S40519|A49321|amyloid beta
(A4) homolog 2 precursor - human
>GNP:Z22572|Z22572_1|H.sapiens CDEI binding protein
mRNA; putative. >GNP:L27631|L27631_1|Human amyloid
precursor-like protein 2 (APLP2) mRNA, complete cds.
>GNP:S60099|S60099_1|APPH=amyloid precursor protein
homolog [human, placenta, mRNA, 3727 nt]; amyloid
precursor protein homolog; This sequence comes from Fig.
2.
Length = 763

Score = 44.5 bits (103), Expect = 5e-05
Identities = 20/67 (29%), Positives = 34/67 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYNRRTSKRCETVFVSGCNGNLNNFKLKIEREVA 90
++I D+K C + G C V R++++ + +C F++ GC GN NNF+ +
Sbjct: 300 KEITHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMVA 359

Query: 91 CVAKYKP 97
C A P
Sbjct: 360 CKAMIPP 366

>GSP:R39674|R39674|C-terminal Kunitz-type protease inhibitor
variant.
Length = 58

Score = 44.5 bits (103), Expect = 5e-05
Identities = 19/53 (35%), Positives = 28/53 (51%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNRRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
D CKL + G+C +++Y+ +K C FV+ GC N FK + E E C
Sbjct: 3 DICKLPKDEGTCKAYIIKWYDPNTKSCARFVYGGCRAKENKFKSQKECEKVC 55

>GSP:R39666|R39666|Human TFPI kunitz-type domain 1-yeast signal
peptide fusion. >RTR:CAA01313|CAA01313|KUNITZ-TYPE
PROTEASE INHIBITOR. >GNP:A17007|A17007_1|variant of
Kunitz-type protease inhibitor domain 1 of TFPI seq ID
No: 7.
Length = 111

Score = 44.5 bits (103), Expect = 5e-05
Identities = 19/63 (30%), Positives = 34/63 (53%)

Query: 29 IAEEKIGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIERE 88
+AE++ + C + G C + R+F+N +++CE F++ GC GN N F+ E +
Sbjct: 46 MAERLEKRMHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESELECK 105

Query: 89 VAC 91
C
Sbjct: 106 KMC 108

>GSP:R53776|R53776|Sequence of human Kunitz-type inhibitor.
Length = 132

Score = 44.5 bits (103), Expect = 5e-05
Identities = 20/67 (29%), Positives = 34/67 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVA 90
++I D+K C + G C V R++++ + +C F++ GC GN NNF+ +
Sbjct: 48 KEITHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMV 107

Query: 91 CVAKYKP 97
C A P
Sbjct: 108 CKAMIPP 114

>GSP:R53778|R53778|Sequence of human amyloid protein precursor
homologue encoded byclone APPH.
>GNP:L09209|L09209_1|Homo sapiens amyloid protein
homologue mRNA, complete cds; homologue; putative.
Length = 763

Score = 44.5 bits (103), Expect = 5e-05
Identities = 20/67 (29%), Positives = 34/67 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVA 90
++I D+K C + G C V R++++ + +C F++ GC GN NNF+ +
Sbjct: 300 KEITHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMV 359

Query: 91 CVAKYKP 97
C A P
Sbjct: 360 CKAMIPP 366

>PIR:A54849 PH0844 S16316 I56328 A30296 I84686|A54849|collagen alpha
1(VII) chain precursor - human
Length = 2944

Score = 44.5 bits (103), Expect = 5e-05
Identities = 23/67 (34%), Positives = 33/67 (48%), Gaps = 8/67 (11%)

Query: 36 DLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACV 92
D DPC L ++ GSC R+++ +++ C FV+ GC GN N F + E C
Sbjct: 2871 DEDDPCSLPLDEGSCTAYTLRWYHRAVTGSTEACHPFVYGGCGGNANRFGTREACERRC- 2929

Query: 93 AKYKPPR 99
PPR
Sbjct: 2930 ----PPR 2932

>STR:AAD47291|AAD47291|Amyloid precursor protein homolog HSD-2.
>GNP:AF168956|AF168956_1|Homo sapiens amyloid precursor
protein homolog HSD-2 mRNA, complete cds.
Length = 763

Score = 44.5 bits (103), Expect = 5e-05
Identities = 20/67 (29%), Positives = 34/67 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVA 90
++I D+K C + G C V R++++ + +C F++ GC GN NNF+ +
Sbjct: 300 KEITHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRNNFESEDYCMV 359

Query: 91 CVAKYKP 97
C A P
Sbjct: 360 CKAMIPP 366

>STR:Q14594|Q14594|BINDING PROTEIN (FRAGMENT).
 >GNP:L23113|L23113_1|Human binding protein mRNA, 3'end;
 putative.
 Length = 523

Score = 44.5 bits (103), Expect = 5e-05
 Identities = 20/67 (29%), Positives = 34/67 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYNRSTSKRCETFVFSGCNGNLNNFKLKIEREVA 90
 ++I D+K C + G C V R++++ + +C F++ GC GN NNF+ +
 Sbjct: 72 KEITHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFIYGGCGGNRRNNFESEDYCMVA 131
 Query: 91 CVAKYKP 97
 C A P
 Sbjct: 132 CKAMIPP 138

>STR:O14895|O14895|KUNITZ-TYPE PROTEASE INHIBITOR.
 >GNP:AF027205|AF027205_1|Homo sapiens Kunitz-type
 protease inhibitor (kop) mRNA, complete cds; KOP;
 contains putative transmembrane domain; similar to
 human placental bikunin; overexpressed in pancreatic
 cancer.
 Length = 252

Score = 44.5 bits (103), Expect = 5e-05
 Identities = 25/69 (36%), Positives = 36/69 (51%), Gaps = 2/69 (2%)

Query: 18 LNTLLLGGVNKKIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNRSTSKRCETFVFSGCNGN 77
 L +LLL GV +A + D C + G C +++YN T C+ FV+ GC+GN
 Sbjct: 17 LGSLLLSGV--LAADRERSIHDFCLVSKVVGRCRASMPKWWYNVTDGSCQLFVYGGCDGN 74
 Query: 78 LNNFKLKIE 86
 NN+ K E
 Sbjct: 75 SNNYLTKEE 83

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYNRSTSKRCETFVFSGCNGNLNNFKLKIEREVACVAKYKPP 98
 C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 133 CTANAVTGPCRASFPWWYFDVERNNSCNFIYGGCRGNKNSYRSEEACMLRCFRQQENP 190

>GSP:R81889|R81889|Kallikrein inhibitor protein KKII/3#2.
 Length = 58

Score = 44.1 bits (102), Expect = 6e-05
 Identities = 18/51 (35%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYNRSTSKRCETFVFSGCNGNLNNFKLKIEREVAC 91
 C + G C H R+F+N +++CE F + GC GN N F+ E + C
 Sbjct: 5 CAFKADDGPCKANHLRFFNFIFTRQCEEFSGCGGNQNRFSLEECKKMC 55

>GSP:R22988|R22988|Aprotinin analogue #13 with reduced
 nephrotoxicity.
 Length = 141

Score = 44.1 bits (102), Expect = 6e-05
 Identities = 21/52 (40%), Positives = 26/52 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYNRSTSKRCETFVFSGCNGNLNNFK 82
 E + D +D C G C RYFYN + C+TFV+ GC NNFK
 Sbjct: 78 EGVSLDKRDFCLEPPYTGPCKARIIRYFYNAEAGLCQTFVYGGCRAKSNNFK 129

>GSP:R22986|R22986|Aprotinin analogue #11 with reduced
 nephrotoxicity.
 Length = 141

Score = 44.1 bits (102), Expect = 6e-05
 Identities = 21/52 (40%), Positives = 26/52 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFGSGCNGNLNNFK 82
 E + D +D C G C RYFYN + C+TFV+ GC NNFK
 Sbjct: 78 EGVSLDKRDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKSNNNFK 129

>GSP:W19803|W19803|Alpha mating factor:KPI(-4-57;I16H,S17W) encoded
 by pTW6185. >GSP:Y68032|Y68032|Yeast
 mating-factor-KPI(-4-57) fusion protein sequence Fig 17.
 Length = 146

Score = 44.1 bits (102), Expect = 6e-05
 Identities = 18/57 (31%), Positives = 31/57 (53%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFGSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C +H+R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 88 VREVCSEQAETGPCRAMHWRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 140

>GSP:W64143|W64143|Human Kunitz-type serine protease inhibitor
 domain #39. >GSP:W64121|W64121|Human Kunitz-type serine
 protease inhibitor domain #17.
 Length = 58

Score = 44.1 bits (102), Expect = 6e-05
 Identities = 16/45 (35%), Positives = 25/45 (55%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFGSGCNGNLNNF 81
 +++ C G C H R++++ T +C FV+ GC GN NNF
 Sbjct: 1 VREVCSEQAETGPCRAAHSRWYFDVTEGKCAPFFYGGCGGNRNNF 45

>GSP:Y68041|Y68041|Kunitz protease inhibitor analogue protein
 sequence Fig 33. >GSP:Y68138|Y68138|Kunitz protease
 inhibitor variant TW6185.
 Length = 61

Score = 44.1 bits (102), Expect = 6e-05
 Identities = 18/57 (31%), Positives = 31/57 (53%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFGSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C +H+R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMHWRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>STR:O95959|O95959|DJ461P17.1 PROTEIN (FRAGMENT).
 Length = 232

Score = 44.1 bits (102), Expect = 6e-05
 Identities = 21/63 (33%), Positives = 33/63 (52%), Gaps = 1/63 (1%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFGSGCNGNLNNFKLKIEREV 89
 +K C D ++PC L + G+C R+ ++ + RC F + GC GN NNF +
 Sbjct: 75 QKKCMDPFQEP CMLPVRHGNCNHEAQRWHFDFKNYRCTPFKYRGCEGNANNFLNEDACRT 134

Query: 90 ACV 92
 AC+
 Sbjct: 135 ACM 137

>GSP:R22987|R22987|Aprotinin analogue #12 with reduced
 nephrotoxicity.
 Length = 141

Score = 43.8 bits (101), Expect = 8e-05
 Identities = 21/52 (40%), Positives = 26/52 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFGSGCNGNLNNFK 82
 E + D +D C G C RYFYN + C+TFV+ GC NNFK
 Sbjct: 78 EGVSLDKRDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKENNNFK 129

>GSP:R22989|R22989|Aprotinin analogue #14 with reduced
 nephrotoxicity.
 Length = 141

Score = 43.8 bits (101), Expect = 8e-05
 Identities = 21/52 (40%), Positives = 26/52 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
 E + D + D C G C RYFYNN + C+TFV+ GC NNFK
 Sbjct: 78 EGVSLDKRDFCLEPPYTGPCKARIIRYFYNAEAGLCQTFVYGGCRAKENNFK 129

>GSP:R39670|R39670|C-terminal Kunitz-type protease inhibitor
 variant.
 Length = 58

Score = 43.8 bits (101), Expect = 8e-05
 Identities = 19/53 (35%), Positives = 28/53 (51%)

Query: 39 DPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 D CKL + G+C +++Y+ +K C FV+ GC N FK + E E C
 Sbjct: 3 DICKLPKDEGTCKARIIKWYYDPNTKSCARFVYGGCRAKENKFSQKECEKVC 55

>GSP:R81931|R81931|Human protease nexin-II Kunitz domain derived
 protein DK1-5.1.
 Length = 58

Score = 43.8 bits (101), Expect = 8e-05
 Identities = 19/57 (33%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C H R++++ T +CE F + GC GN NNF + E C+A
 Sbjct: 1 VREVCSEQAETGPCRAAHPRWYFDVTEGKCEEFSGCGGNRNNF----DTEEYCMA 53

>GSP:R81905|R81905|Kallikrein inhibitor protein KK2/#1.
 Length = 58

Score = 43.8 bits (101), Expect = 8e-05
 Identities = 18/51 (35%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C H R+F+N +++CE F + GC GN N F+ E + C
 Sbjct: 5 CAFKADVGRGCRGAHPRWFFNIFTRQCEEFSGCGGNQNRFSLEECKKMC 55

>GSP:W64145|W64145|Human Kunitz-type serine protease inhibitor
 domain #41.
 Length = 58

Score = 43.8 bits (101), Expect = 8e-05
 Identities = 16/45 (35%), Positives = 25/45 (55%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNF 81
 +++ C G C H R++++ T +C FV+ GC GN NNF
 Sbjct: 1 VREVCSEQAETGPCRGAHSRWYFDVTEGKCAPFVYGGCGGNRNNF 45

>GSP:R81890|R81890|Kallikrein inhibitor protein KKII/3#3.
 Length = 58

Score = 43.8 bits (101), Expect = 8e-05
 Identities = 18/51 (35%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C H R+F+N +++CE F + GC GN N F+ E + C
 Sbjct: 5 CAFKADDGHCKANHQRFFNIFTRQCEEFYGGCGGNQNRFSLEECKKMC 55

>GSP:R39664|R39664|Human TFPI kunitz-type protease inhibitor
 domain I. >GSP:R81886|R81886|Lipoprotein-associated
 coagulation inhibitor Kunitz domain LACI-K1.
 >GSP:R99185|R99185|Human aprotinin-like Kunitz domain
 (LACI-D1). >GSP:W64112|W64112|Human Kunitz-type serine
 protease inhibitor domain #8.
 >GSP:W92859|W92859|US5880256 Seq ID 35.
 >RTR:E973997|E973997|KUNITZ-TYPE PROTEASE INHIBITOR
 DOMAIN 1 OF TFPI SEQ ID NO: 4.
 Length = 58

Score = 43.4 bits (100), Expect = 1e-04
 Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C + R+F+N +++CE F++ GC GN N F+ E + C
 Sbjct: 5 CAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 55

>GSP:R81903|R81903|Kallikrein inhibitor protein KK2/#5.
 >GSP:R81904|R81904|Kallikrein inhibitor protein
 KK2/#11.
 Length = 58

Score = 43.4 bits (100), Expect = 1e-04
 Identities = 18/51 (35%), Positives = 27/51 (52%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C H R+F+N +++CE F + GC GN N F+ E + C
 Sbjct: 5 CAFKADDGPCRAAHPRWFFNIFTRQCEEFYGGCGGNQNRFSLEECKKMC 55

>GSP:R92257|R92257|TFPI first Kunitz-type domain.
 Length = 51

Score = 43.4 bits (100), Expect = 1e-04
 Identities = 17/51 (33%), Positives = 28/51 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVAC 91
 C + G C + R+F+N +++CE F++ GC GN N F+ E + C
 Sbjct: 1 CAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFSLEECKKMC 51

>GSP:W19805|W19805|Alpha mating factor:KPI(-4-57;M15L,I16H) encoded
 by pTW6174. >GSP:Y68034|Y68034|Yeast
 mating-factor-KPI(-4-57) fusion protein sequence Fig 19.
 Length = 146

Score = 43.0 bits (99), Expect = 1e-04
 Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C +H R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 88 VREVCSEQAETGPCRALHSRWYFDVTEGKCAPFFYGGCGGNRNNF---DTEEYCMA 140

>GSP:W18411|W18411|KPI(-4 to 57) I16H. >GSP:Y68075|Y68075|Kunitz
 protease inhibitor variant TW6172.
 Length = 61

Score = 43.0 bits (99), Expect = 1e-04
 Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C +H R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMHSRWYFDVTEGKCAPFFYGGCGGNRNNF---DTEEYCMA 55

>GSP:W64123|W64123|Human Kunitz-type serine protease inhibitor
 domain #19.
 Length = 58

Score = 43.0 bits (99), Expect = 1e-04
 Identities = 16/45 (35%), Positives = 25/45 (55%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNF 81
 +++ C G C H R++++ T +C FV+ GC GN NNF
 Sbjct: 1 VREVCSEQAEDGHCRAAHPRWYFDVTEGKCAPFVYGGCGGNRNNF 45

>GSP:W64129|W64129|Human Kunitz-type serine protease inhibitor
 domain #25.
 Length = 58

Score = 43.0 bits (99), Expect = 1e-04
 Identities = 16/45 (35%), Positives = 25/45 (55%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNF 81
 +++ C G C H R++++ T +C FV+ GC GN NNF
 Sbjct: 1 VREVCSEQAEEGHCRAAHPRWYFDVTEGKCAPFVYGGCGGNRNNF 45

>GSP:Y68044|Y68044|Kunitz protease inhibitor analogue protein
sequence Fig 36. >GSP:Y68119|Y68119|Kunitz protease
inhibitor variant TW6174.
Length = 61

Score = 43.0 bits (99), Expect = 1e-04
Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C +H R++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRALHSRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>PIR:S41082|S41082|amyloid precursor protein homolog - human
(fragment)
Length = 111

Score = 43.0 bits (99), Expect = 1e-04
Identities = 21/61 (34%), Positives = 32/61 (52%), Gaps = 4/61 (6%)

Query: 36 DLKDPCKLDMNFGSCYEVHFRYFYNRRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKY 95
D+K C + G C V R++++ + +C F++ GC GN NNF E E C+A
Sbjct: 54 DVKAVCSQEAMTGPCRAVMRWYFDLSKGKCVRFIYGGCGGNRNNF----ESEDYCMAYC 109

Query: 96 K 96
K
Sbjct: 110 K 110

>GSP:W19804|W19804|Alpha mating factor:KPI(-4-57;M15A,I16H) encoded
by pTW6173. >GSP:Y68033|Y68033|Yeast
mating-factor-KPI(-4-57) fusion protein sequence Fig 18.
Length = 146

Score = 42.6 bits (98), Expect = 2e-04
Identities = 18/57 (31%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C H R++++ T +C F + GC GN NNF + E C+A
Sbjct: 88 VREVCSEQAETGPCRAAHSRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 140

>GSP:W64147|W64147|Human Kunitz-type serine protease inhibitor
domain #43. >GSP:W64120|W64120|Human Kunitz-type serine
protease inhibitor domain #16.
Length = 58

Score = 42.6 bits (98), Expect = 2e-04
Identities = 15/45 (33%), Positives = 25/45 (55%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRRTSKRCETVFVSGCNGNLNNF 81
+++ C G C +H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAETGPCRALHSRWYFDVTEGKCAPFFYGGCGGNRNNF 45

>GSP:W64126|W64126|Human Kunitz-type serine protease inhibitor
domain #22.
Length = 58

Score = 42.6 bits (98), Expect = 2e-04
Identities = 16/45 (35%), Positives = 25/45 (55%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRRTSKRCETVFVSGCNGNLNNF 81
+++ C G C H R++++ T +C FV+ GC GN NNF
Sbjct: 1 VREVCSEQAEPGHCRAAHPRWYFDVTEGKCAPFVYGGCGGNRNNF 45

>GSP:Y68043|Y68043|Kunitz protease inhibitor analogue protein
sequence Fig 35. >GSP:Y68118|Y68118|Kunitz protease
inhibitor variant TW6173.
Length = 61

Score = 42.6 bits (98), Expect = 2e-04
Identities = 18/57 (31%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C H R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAAHSRWYFDVTEGKCAPFFYGGCGNRNNF----DTEEYCMA 55

>GSP:Y68146|Y68146|Kunitz protease inhibitor variant DD170.
 Length = 61

Score = 42.6 bits (98), Expect = 2e-04
 Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C +H R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRALHNRWYFDVTEGKCAPFFYGGCGNRNNF----DTEEYCMA 55

>GSP:Y68176|Y68176|Kunitz protease inhibitor variant DD118.
 Length = 61

Score = 42.6 bits (98), Expect = 2e-04
 Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C +H R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRALHNRWYFDVTEGKCAPFFYGGCGNRNNF----DTEEYCMA 55

>GSP:R22981|R22981|Aprotinin analogue #6 with reduced
 nephrotoxicity.
 Length = 141

Score = 42.6 bits (98), Expect = 2e-04
 Identities = 20/52 (38%), Positives = 26/52 (49%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFK 82
 E + D +D C G C RYFYN + C+TFV+ GC NNF+
 Sbjct: 78 EGVSLDKRDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKSNNFE 129

>GSP:R22982|R22982|Aprotinin analogue #7 with reduced
 nephrotoxicity.
 Length = 141

Score = 42.2 bits (97), Expect = 2e-04
 Identities = 20/51 (39%), Positives = 25/51 (48%)

Query: 31 EKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFK 81
 E + D +D C G C RYFYN + C+TFV+ GC NNF
 Sbjct: 78 EGVSLDKRDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKSNNFE 128

>GSP:W18431|W18431|KPI(-4 to 57) I16H, G38Y.
 >GSP:Y68140|Y68140|Kunitz protease inhibitor variant
 TW6186.
 Length = 61

Score = 42.2 bits (97), Expect = 2e-04
 Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C +H R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMHSRWYFDVTEGKCAPFFYGGCYGNRNNF----DTEEYCMA 55

>GSP:W30053|W30053|Human placental bikunin.
 Length = 179

Score = 42.2 bits (97), Expect = 2e-04
 Identities = 19/50 (38%), Positives = 27/50 (54%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIE 86
 + D C + G C R++YN T C+ FV+ GC+GN NN+ K E
 Sbjct: 7 IHDFCLVSKVVGRCRASMPRWYNVTDGSCQLFVYGGCDGNSNNYLTKEE 56

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPP 98
 C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 106 CTANAVTGPCRASFPWWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQENP 163

>GSP:W30054|W30054|Human placental bikunin.
 Length = 92

Score = 42.2 bits (97), Expect = 2e-04
 Identities = 19/50 (38%), Positives = 27/50 (54%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIE 86
 + D C + G C R++YN T C+ FV+ GC+GN NN+ K E
 Sbjct: 7 IHDFCLVSKVVGRCRASMPPWWYNVTDGSCQLFVYGGCDGNSNNYLTKEE 56

>GSP:W30041|W30041|Human placental bikunin.
 Length = 170

Score = 42.2 bits (97), Expect = 2e-04
 Identities = 19/50 (38%), Positives = 27/50 (54%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIE 86
 + D C + G C R++YN T C+ FV+ GC+GN NN+ K E
 Sbjct: 7 IHDFCLVSKVVGRCRASMPPWWYNVTDGSCQLFVYGGCDGNSNNYLTKEE 56

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPP 98
 C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 106 CTANAVTGPCRASFPWWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQENP 163

>GSP:W30042|W30042|Human placental bikunin.
 Length = 213

Score = 42.2 bits (97), Expect = 2e-04
 Identities = 19/50 (38%), Positives = 27/50 (54%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIE 86
 + D C + G C R++YN T C+ FV+ GC+GN NN+ K E
 Sbjct: 7 IHDFCLVSKVVGRCRASMPPWWYNVTDGSCQLFVYGGCDGNSNNYLTKEE 56

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPP 98
 C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 106 CTANAVTGPCRASFPWWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQENP 163

>GSP:W30046|W30046|Human placental bikunin.
 Length = 225

Score = 42.2 bits (97), Expect = 2e-04
 Identities = 19/50 (38%), Positives = 27/50 (54%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIE 86
 + D C + G C R++YN T C+ FV+ GC+GN NN+ K E
 Sbjct: 7 IHDFCLVSKVVGRCRASMPPWWYNVTDGSCQLFVYGGCDGNSNNYLTKEE 56

Score = 33.6 bits (75), Expect = 0.090
 Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPP 98
 C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 106 CTANAVTGPCRASFPWWYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQENP 163

>GSP:W30047|W30047|Human placental bikunin.
 Length = 58

Score = 42.2 bits (97), Expect = 2e-04
Identities = 19/50 (38%), Positives = 27/50 (54%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIE 86
+ D C + G C R++YN T C+ FV+ GC+GN NN+ K E
Sbjct: 1 IHDFCLVSKVVGRCRASMPRWYNNVTDGSCQLFVYGGCDGNSNNYLTKEE 50

>GSP:W27368|W27368|Hepatocyte growth factor activator inhibitor.
>GSP:W92653|W92653|Human HAI-1 protein.
>STR:O43278|O43278|HEPATOCYTE GROWTH FACTOR ACTIVATOR
INHIBITOR. >GNP:AB000095|AB000095_1|Homo sapiens mRNA
for hepatocyte growth factor activator inhibitor,
complete cds.
Length = 513

Score = 42.2 bits (97), Expect = 2e-04
Identities = 19/54 (35%), Positives = 30/54 (55%)

Query: 38 KDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVAC 91
+D C G C R++Y+ T + C++FV+ GC GN NN+ + E +AC
Sbjct: 247 EDYCLASNKVGRCRGSFPRWYDPTTEQICKSFVYGGCLGNKNNYLREEECILAC 300

Score = 40.2 bits (92), Expect = 0.001
Identities = 23/59 (38%), Positives = 28/59 (46%), Gaps = 11/59 (18%)

Query: 34 CGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACV 92
C DL D G C E R++YN S+ C F + GC GN NNF E E C+
Sbjct: 375 CVDLPDT-----GLCKESIPRWYNNPFSEHCARFTYGGCYGNKNF---EEEQQL 422

>GSP:W30051|W30051|Human placental bikunin.
Length = 153

Score = 42.2 bits (97), Expect = 2e-04
Identities = 19/50 (38%), Positives = 27/50 (54%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIE 86
+ D C + G C R++YN T C+ FV+ GC+GN NN+ K E
Sbjct: 1 IHDFCLVSKVVGRCRASMPRWYNNVTDGSCQLFVYGGCDGNSNNYLTKEE 50

Score = 33.2 bits (74), Expect = 0.12
Identities = 14/54 (25%), Positives = 26/54 (47%), Gaps = 4/54 (7%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVAK 94
C + G C R++++ C F++ GC GN N+++ E AC+ +
Sbjct: 100 CTANAVTGPCRASFRWYFDVERNSCNNFIYGGCRGNKNSYR----SEEACMLR 149

>GSP:W64144|W64144|Human Kunitz-type serine protease inhibitor
domain #40.
Length = 58

Score = 42.2 bits (97), Expect = 2e-04
Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNF 81
+++ C G C H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAETGPCRAAHSRWYFDVTEGKCAPFYGGCGGNRNNF 45

>GSP:Y52594|Y52594|Wild-type human Kunitz domain, zkun5.
Length = 62

Score = 42.2 bits (97), Expect = 2e-04
Identities = 20/56 (35%), Positives = 31/56 (54%), Gaps = 1/56 (1%)

Query: 38 KDP-CKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACV 92
+DP C + G+C E R++Y++ C F FSGCNG+ N F + E + C+
Sbjct: 5 EDPRCLEALKPGNCGEYVVRWYDQVNSCARFWFSGCNGSGNRFNSEKECQETCI 60

>GSP:Y52597|Y52597|Human zkun5 protein (portion).
Length = 557

Score = 42.2 bits (97), Expect = 2e-04
Identities = 20/56 (35%), Positives = 31/56 (54%), Gaps = 1/56 (1%)

Query: 38 KDP-CKLDMNFGSCYEVHFRYFYNRSTSKRCETFFVSGCNGNLNNFKLKIIEVACV 92
+DP C + G+C E R++Y++ C F FSGCNG+ N F + E + C+
Sbjct: 500 EDPRCLEALKPGNCGEYVVRWYDQVNSCARFWFSGCNGSGNRFNSEKECQETCI 555

>GSP:R39792|R39792|Human Kunitz-type protease inhibitor.
Length = 60

Score = 41.8 bits (96), Expect = 3e-04
Identities = 19/55 (34%), Positives = 27/55 (48%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRSTSKRCETFFVSGCNGNLNNFKLKIIEVAC 91
L + C M G C R+F++ + CE F + GC GN +NF K + E C
Sbjct: 3 LPNVCAFPMEKGPCQTYMTRWFFDFETGECELFAYGGCGGNSDNFLRKEKCEKFC 57

>GSP:W18449|W18449|Alpha mating factor:KPI(-4-57;M15L,S17F) encoded
by pTW6175. >GSP:Y68028|Y68028|Yeast
mating-factor-KPI(-4-57) fusion protein sequence Fig 13.
Length = 146

Score = 41.8 bits (96), Expect = 3e-04
Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRSTSKRCETFFVSGCNGNLNNFKLKIIEVACVA 93
+++ C G C + FR++++ T +C F + GC GN NNF + E C+A
Sbjct: 88 VREVCSEQAETGPCRALIFRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 140

>GSP:W18418|W18418|KPI(-4 to 57) S17F. >GSP:Y68081|Y68081|Kunitz
protease inhibitor variant DD103.
Length = 61

Score = 41.8 bits (96), Expect = 3e-04
Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRSTSKRCETFFVSGCNGNLNNFKLKIIEVACVA 93
+++ C G C + FR++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMIFRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68037|Y68037|Kunitz protease inhibitor analogue protein
sequence Fig 29. >GSP:Y68128|Y68128|Kunitz protease
inhibitor variant TW6175.
Length = 61

Score = 41.8 bits (96), Expect = 3e-04
Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRSTSKRCETFFVSGCNGNLNNFKLKIIEVACVA 93
+++ C G C + FR++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRALIFRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W18426|W18426|KPI(-4 to 57) M15A, S17F.
>GSP:Y68042|Y68042|Kunitz protease inhibitor analogue
protein sequence Fig 34. >GSP:Y68122|Y68122|Kunitz
protease inhibitor variant DD185.
Length = 61

Score = 41.4 bits (95), Expect = 4e-04
Identities = 18/57 (31%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNRSTSKRCETFFVSGCNGNLNNFKLKIIEVACVA 93
+++ C G C FR++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAAIFRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W19809|W19809|Alpha mating factor:KPI(-4-57;M15A,S17F) encoded
by pDD185. >GSP:Y68048|Y68048|Yeast
mating-factor-KPI(-4-57) fusion protein sequence Fig 62.
Length = 146

Score = 41.4 bits (95), Expect = 4e-04

Identities = 18/57 (31%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C FR++++ T +C F + GC GN NNF + E C+A
 Sbjct: 88 VREVCSEQAETGPCRAAIFRWYFDVTEGKCAPFFYGGCGGNRRNF----DTEEYCMA 140

>GSP:W18551|W18551|Kunitz type active site inhibitor domain
 IV-40B. >GSP:W92894|W92894|US5880256 Seq ID 70.
 >GSP:W94239|W94239|Serine protease mutant inhibitor
 IV-40B. >GSP:W72816|W72816|Mutant inhibitor IV-40B.
 Length = 58

Score = 41.4 bits (95), Expect = 4e-04
 Identities = 14/45 (31%), Positives = 27/45 (59%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNF 81
 +++ C G+C ++ R++++ T +C F++ GC GN NNF
 Sbjct: 1 VREVCSEQAEPGACKAMYKRWFYFDVTEGKCAPFIYGGCGGNRRNF 45

>GSP:Y68149|Y68149|Kunitz protease inhibitor variant BG006.
 Length = 61

Score = 41.4 bits (95), Expect = 4e-04
 Identities = 18/57 (31%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C FR++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAALFRWYFDVTEGKCAPFFYGGCGGNRRNF----DTEEYCMA 55

>GSP:Y68163|Y68163|Kunitz protease inhibitor variant DD116.
 Length = 61

Score = 41.4 bits (95), Expect = 4e-04
 Identities = 18/57 (31%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C FR++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAAIFRWYFDVTEGKCAPFFYGGCGGNRRNF----DTEEYCMA 55

>GSP:W30052|W30052|Human placental bikunin.
 Length = 146

Score = 41.0 bits (94), Expect = 5e-04
 Identities = 18/46 (39%), Positives = 25/46 (54%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIE 86
 C + G C R++YN T C+ FV+ GC+GN NN+ K E
 Sbjct: 1 CLVSKVVGRCRASMPRWYNVTDGSCQLFVYGGCDGNSNNYLTKEE 46

Score = 33.2 bits (74), Expect = 0.12
 Identities = 14/54 (25%), Positives = 26/54 (47%), Gaps = 4/54 (7%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVAK 94
 C + G C R++++ C F++ GC GN N+++ E AC+ +
 Sbjct: 96 CTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCGGNKNSYR---SEEACMLR 145

>GSP:W64146|W64146|Human Kunitz-type serine protease inhibitor
 domain #42.
 Length = 58

Score = 41.0 bits (94), Expect = 5e-04
 Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNF 81
 +++ C G C H R++++ T +C F + GC GN NNF
 Sbjct: 1 VREVCSEQAETGPCRGAHSRWYFDVTEGKCAPFWYGGCGGNRRNF 45

>GSP:W64122|W64122|Human Kunitz-type serine protease inhibitor
 domain #18.
 Length = 58

Score = 41.0 bits (94), Expect = 5e-04
Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNF 81
+++ C G C H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAEDGHCRAAHPRWYFDVTEGKCAPFFYGGCGNRNNF 45

>GSP:W64124|W64124|Human Kunitz-type serine protease inhibitor
domain #20.
Length = 58

Score = 41.0 bits (94), Expect = 5e-04
Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNF 81
+++ C G C H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAEDGHCRAAHPRWYFDVTEGKCAPFFYGGCGNRNNF 45

>GSP:W64128|W64128|Human Kunitz-type serine protease inhibitor
domain #24.
Length = 58

Score = 41.0 bits (94), Expect = 5e-04
Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNF 81
+++ C G C H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAEEGHCRAAHPRWYFDVTEGKCAPFFYGGCGNRNNF 45

>GSP:W64130|W64130|Human Kunitz-type serine protease inhibitor
domain #26.
Length = 58

Score = 41.0 bits (94), Expect = 5e-04
Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNF 81
+++ C G C H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAEEGHCRAAHPRWYFDVTEGKCAPFFYGGCGNRNNF 45

>GSP:Y68100|Y68100|Kunitz protease inhibitor variant TW6140.
Length = 61

Score = 41.0 bits (94), Expect = 5e-04
Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + R++++ T +C F + GCNGN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCNGNRNNF---DTEEYCMA 55

>GSP:Y68141|Y68141|Kunitz protease inhibitor variant TW6187.
Length = 61

Score = 41.0 bits (94), Expect = 5e-04
Identities = 18/57 (31%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + FR++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMIFRWYFDVTEGKCAPFFYGGCYGNRRNF---DTEEYCMA 55

>GSP:R22978|R22978|Aprotinin analogue #3 with reduced
nephrotoxicity.
Length = 111

Score = 40.6 bits (93), Expect = 7e-04
Identities = 20/54 (37%), Positives = 27/54 (49%)

Query: 29 IAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
+AE++ D C G C RYFYN + C+TFV+ GC NNF+
Sbjct: 46 MAERLEKRRPDFCLEPPYTGPCKARIIRYFYNAGLCQTFVYGGCRAKENNFE 99

>GSP:R22976|R22976|Aprotinin analogue #1 with reduced
nephrotoxicity.
Length = 111

Score = 40.6 bits (93), Expect = 7e-04
Identities = 20/54 (37%), Positives = 27/54 (49%)

Query: 29 IAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
+AE++ D C G C RYFYN + C+TFV+ GC NNF+
Sbjct: 46 MAERLEKREPDFCLEPPYTGPCKARIIRYFYNAEAGLCQTFVYGGCRAERNNFE 99

>GSP:R22980|R22980|Aprotinin analogue #5 with reduced
nephrotoxicity.
Length = 111

Score = 40.6 bits (93), Expect = 7e-04
Identities = 20/53 (37%), Positives = 27/53 (50%)

Query: 29 IAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 81
+AE++ D C + G C YFYN + C+TFV+ GC GN N F
Sbjct: 46 MAERLEKRRPDFCLEPPSTGPCKARIILYFYNAKAGLCQTFVYGGCRGNGNQF 98

>GSP:W18450|W18450|Alpha mating factor:KPI(-4-57;M15L,S17Y) encoded
by pBG028. >GSP:Y68029|Y68029|Yeast
mating-factor-KPI(-4-57) fusion protein sequence Fig 14.
Length = 146

Score = 40.6 bits (93), Expect = 7e-04
Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + +R++++ T +C F + GC GN NNF + E C+A
Sbjct: 88 VREVCSEQAETGPCRALIYRWYFDVTEGKCAPFFYGGCGGNRRNF----DTEEYCMA 140

>GSP:W18419|W18419|KPI(-4 to 57) S17Y. >GSP:Y68082|Y68082|Kunitz
protease inhibitor variant DD104.
Length = 61

Score = 40.6 bits (93), Expect = 7e-04
Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + +R++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMIYRWYFDVTEGKCAPFFYGGCGGNRRNF----DTEEYCMA 55

>GSP:W64148|W64148|Human Kunitz-type serine protease inhibitor
domain #44.
Length = 58

Score = 40.6 bits (93), Expect = 7e-04
Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 81
+++ C G C H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAETGPCRANHRSRWYFDVTEGKCAPFFYGGCGGNRRNF 45

>GSP:W64125|W64125|Human Kunitz-type serine protease inhibitor
domain #21.
Length = 58

Score = 40.6 bits (93), Expect = 7e-04
Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 81
+++ C G C H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAEPGHCRAAHPRWYFDVTEGKCAPFFYGGCGGNRRNF 45

>GSP:W64127|W64127|Human Kunitz-type serine protease inhibitor
domain #23.

Length = 58

Score = 40.6 bits (93), Expect = 7e-04
Identities = 15/45 (33%), Positives = 24/45 (53%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNF 81
+++ C G C H R++++ T +C F + GC GN NNF
Sbjct: 1 VREVCSEQAEPGHCRAAHPRWYFDVTEGKCAPFFYGGCGGNRNNF 45

>GSP:Y68038|Y68038|Kunitz protease inhibitor analogue protein
sequence Fig 30. >GSP:Y68125|Y68125|Kunitz protease
inhibitor variant BG028.
Length = 61

Score = 40.6 bits (93), Expect = 7e-04
Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + +R++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRALIYRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68164|Y68164|Kunitz protease inhibitor variant TW6191.
Length = 61

Score = 40.6 bits (93), Expect = 7e-04
Identities = 18/57 (31%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C FR++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAAIFRWYFDVTEGKCAPFFYGGCYGNRNNF----DTEEYCMA 55

>STR:O95428|O95428|HYPOTHETICAL 133.5 KDA PROTEIN.
>GNP:AF109907|AF109907_3|Homo sapiens S164 gene, partial
cds; PS1 and hypothetical protein genes, complete cds; .
and S171 gene, partial cds; This gene is predicted by
Genscan; exons between 169766-172443 are supported by
EST AA930352; exons between 183120-186473 are supported
by EST AA763659; Blastx gives greatest similarity to
predicted proteins from U64857 in C. elegans; this
hypothetical protein contains thrombospondin motifs and
is partially similar to robo1 (roundabout).
Length = 1235

Score = 40.6 bits (93), Expect = 7e-04
Identities = 19/59 (32%), Positives = 29/59 (48%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPPR 99
C L GSC + R+++ + +C F + GC+GN NNF + E +C PR
Sbjct: 692 CLLPSAHGSCADWAARWYFVASVGQCNRFWYGGCHGNANNFASEQECMSSCQGLHGPR 750

>GSP:R22977|R22977|Aprotinin analogue #2 with reduced
nephrotoxicity.
Length = 111

Score = 40.2 bits (92), Expect = 0.001
Identities = 20/54 (37%), Positives = 27/54 (49%)

Query: 29 IAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFK 82
+AE++ D C G C RYFYNN + C+TFV+ GC NNF+
Sbjct: 46 MAERLEKREPDPFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKENNFE 99

>GSP:W18448|W18448|Alpha mating factor:KPI(-4-57;M15A,S17Y) encoded
by pTW6166. >GSP:Y68027|Y68027|Yeast
mating-factor-KPI(-4-57) fusion protein sequence Fig 12.
Length = 146

Score = 40.2 bits (92), Expect = 0.001
Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C +R++++ T +C F + GC GN NNF + E C+A
Sbjct: 88 VREVCSEQAETGPCRAAIIYRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 140

>GSP:W18427|W18427|KPI(-4 to 57) M15A, S17Y.
 >GSP:Y68036|Y68036|Kunitz protease inhibitor analogue
 protein sequence Fig 28. >GSP:Y68124|Y68124|Kunitz
 protease inhibitor variant TW6166.
 Length = 61

Score = 40.2 bits (92), Expect = 0.001
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIERYVACVA 93
 +++ C G C +R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAAIYRWYFDVTEGKCAPFFYGGCGGNRRNF----DTEECMA 55

>GSP:W19808|W19808|phoA:KIP(1-55;M15A,S17F):geneIII fusion.
 >GSP:Y68047|Y68047|PhoA-KPI (155)-geneIII fusion
 protein sequence Fig 60.
 Length = 233

Score = 40.2 bits (92), Expect = 0.001
 Identities = 18/53 (33%), Positives = 26/53 (48%), Gaps = 4/53 (7%)

Query: 41 CKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIERYVACVA 93
 C G C FR++++ T +C F + GC GN NNF + E C+A
 Sbjct: 24 CSEQAETGPCRAAIFRWYFDVTEGKCAPFFYGGCGGNRRNF----DTEECMA 72

>GSP:W63684|W63684|Human secreted protein 4.
 Length = 206

Score = 40.2 bits (92), Expect = 0.001
 Identities = 23/59 (38%), Positives = 28/59 (46%), Gaps = 11/59 (18%)

Query: 34 CGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIERYVACV 92
 C DL D G C E R++YN S+ C F + GC GN NNF E E C+
 Sbjct: 68 CVDLPDT-----GLCKESIPRWYNNPFSEHCARFTYGGCYGNKNNF----EEEQQL 115

>GSP:Y68062|Y68062|Kunitz protease inhibitor variant TW6167.
 Length = 61

Score = 40.2 bits (92), Expect = 0.001
 Identities = 18/66 (27%), Positives = 33/66 (49%), Gaps = 11/66 (16%)

Query: 28 KIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIERY 87
 ++ ++C + +PC C + R++++ T +C F + GC GN NNF +
 Sbjct: 1 EVVREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRRNF----DT 49

Query: 88 EVACVA 93
 E C+A
 Sbjct: 50 EECMA 55

>GSP:W18444|W18444|Alpha mating factor:KPI(1-57) encoded by
 plasmid pKPI-57. >GSP:Y68022|Y68022|KPI (1-57) and a
 yeast mating factor peptide fusion protein.
 Length = 61

Score = 39.9 bits (91), Expect = 0.001
 Identities = 18/58 (31%), Positives = 29/58 (49%), Gaps = 4/58 (6%)

Query: 36 DLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIERYVACVA 93
 D ++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 2 DKREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRRNF----DTEECMA 55

>GSP:W18420|W18420|KPI(-4 to 57) S17W. >GSP:Y68083|Y68083|Kunitz
 protease inhibitor variant DD105.
 Length = 61

Score = 39.9 bits (91), Expect = 0.001
 Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETVFVSGCNGNLNNFKLKIERYVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A

Sbjct: 3 VREVCSEAETGPCRAMIWRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W18557|W18557|Novel fusion protein TFKD1.
Length = 282

Score = 39.9 bits (91), Expect = 0.001
Identities = 15/47 (31%), Positives = 25/47 (52%)

Query: 35 GDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNF 81
G +++ C G C + R++++ T +C F + GC GN NNF
Sbjct: 223 GSVREVCSEAEPGPCRALILRWYFDVTEGKCAPFFYGGCYGNRNNF 269

>GSP:Y68073|Y68073|Kunitz protease inhibitor variant TW6179.
Length = 61

Score = 39.9 bits (91), Expect = 0.001
Identities = 18/57 (31%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNF 93
+++ C G C V R++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEAETGPCRAVISRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68142|Y68142|Kunitz protease inhibitor variant TW6188.
Length = 61

Score = 39.9 bits (91), Expect = 0.001
Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNF 93
+++ C G C + R++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEAETGPCRAMIYRWYFDVTEGKCAPFFYGGCYGNRNNF----DTEEYCMA 55

>GSP:Y68144|Y68144|Kunitz protease inhibitor variant TW6170.
Length = 61

Score = 39.9 bits (91), Expect = 0.001
Identities = 18/66 (27%), Positives = 33/66 (49%), Gaps = 11/66 (16%)

Query: 28 KIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNF 87
++ ++C + +P G C + R++++ T +C F + GC GN NNF +
Sbjct: 1 EVVREVCSEAEP-----GPCRALILRWYFDVTEGKCAPFFYGGCGGNRNNF----DT 49

Query: 88 EVACVA 93
E C+A
Sbjct: 50 EECMA 55

>GSP:Y52595|Y52595|Gly20Ala mutant human zkun5 Kunitz domain.
Length = 62

Score = 39.9 bits (91), Expect = 0.001
Identities = 19/56 (33%), Positives = 30/56 (52%), Gaps = 1/56 (1%)

Query: 38 KDP-CKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNF 92
+DP C + G+C R++Y++ C F FSGCNG+ N F + E + C+
Sbjct: 5 EDPRCLEALKPGNCGAYVVRWYDKQVNSCARFWFSGCNGSGNRFNSEKECQETCI 60

>GSP:W18447|W18447|Alpha mating factor:KPI(-4-57;M15A,S17W) encoded
by pTW6165. >GSP:Y68026|Y68026|Yeast
mating-factor-KPI(-4-57) fusion protein sequence Fig 10.
Length = 146

Score = 39.5 bits (90), Expect = 0.002
Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFVFSGCNGNLNNF 93
+++ C G C + R++++ T +C F + GC GN NNF + E C+A
Sbjct: 88 VREVCSEAETGPCRAAIWRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 140

>GSP:W18422|W18422|KPI(-4 to 57) S17L. >GSP:Y68084|Y68084|Kunitz
protease inhibitor variant TW6168.

Length = 61

Score = 39.5 bits (90), Expect = 0.002

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMILRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W18428|W18428|KPI(-4 to 57) M15A, S17W.

>GSP:Y68035|Y68035|Kunitz protease inhibitor analogue
 protein sequence Fig 27. >GSP:Y68123|Y68123|Kunitz
 protease inhibitor variant TW6165.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAAIWRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W18413|W18413|KPI(-4 to 57) I16F. >GSP:Y68077|Y68077|Kunitz
 protease inhibitor variant TW6181.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMFSRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W18414|W18414|KPI(-4 to 57) I16K. >GSP:Y68078|Y68078|Kunitz
 protease inhibitor variant BG001.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMKSRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W18416|W18416|KPI(-4 to 57) S17I.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMIIRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68069|Y68069|Kunitz protease inhibitor variant DD109.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAIISRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68093|Y68093|Kunitz protease inhibitor variant TW6142.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002

Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93

+++ C G C + R++++ T +C F++ GC GN NNF + E C+A
 Sbjct: 3 VREVCSEAETGPCRAMISRWFYFDVTEGKCAPFLYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68121|Y68121|Kunitz protease inhibitor variant DD129.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A

Sbjct: 3 VREVCSEAETGPCRALFSRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68126|Y68126|Kunitz protease inhibitor variant TW6169.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A

Sbjct: 3 VREVCSEAETGPCRALILRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68150|Y68150|Kunitz protease inhibitor variant DD130.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A

Sbjct: 3 VREVCSEAETGPCRALFTRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68156|Y68156|Kunitz protease inhibitor variant DD122.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + F++++ T +C F + GC GN NNF + E C+A

Sbjct: 3 VREVCSEAETGPCRALIFAWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68161|Y68161|Kunitz protease inhibitor variant BG024.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002
 Identities = 16/57 (28%), Positives = 30/57 (52%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + +++++ T +C F + GC GN NNF + E C+A

Sbjct: 3 VREVCSEAETGPCRALIYKWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68170|Y68170|Kunitz protease inhibitor variant BG040.
 Length = 61

Score = 39.5 bits (90), Expect = 0.002
 Identities = 16/57 (28%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + + +++++ T +C F + GC GN NNF + E C+A

Sbjct: 3 VREVCSEAETGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:P94777|P94777|Plasmid pSVMT-APPI carrying novel amyloid
 precursor protein (NAP). >GSP:R06868|R06868|Sequence
 deduced from insert of plasmid pSVMT-APPI.
 Length = 111

Score = 39.1 bits (89), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 37 MREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 89

>GSP:R05167|R05167|Sequence of amyloid precursor protein (APP).
 Length = 62

Score = 39.1 bits (89), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 2 VREVCSSQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 54

>GSP:R08109|R08109|Protein sDOG deduced from insert of plasmid
 pSVMT-DOG.
 Length = 111

Score = 39.1 bits (89), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 37 MREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 89

>GSP:R08110|R08110|Protein sDJ deduced from insert of plasmid
 pSVMT-DJ.
 Length = 94

Score = 39.1 bits (89), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 37 MREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 89

>GSP:W18396|W18396|KPI(-4 to 57) R40A. >GSP:Y68117|Y68117|Kunitz
 protease inhibitor variant TW6149.
 Length = 61

Score = 39.1 bits (89), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNANNF----DTEEYCMA 55

>GSP:W18424|W18424|KPI(-4 to 57) S17H.
 Length = 61

Score = 39.1 bits (89), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMIHRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W18430|W18430|KPI(-4 to 57) M15G, S17Y.
 >GSP:Y68129|Y68129|Kunitz protease inhibitor variant
 TW6201.
 Length = 61

Score = 39.1 bits (89), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAGIYRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:W18412|W18412|KPI(-4 to 57) I16A. >GSP:Y68076|Y68076|Kunitz
protease inhibitor variant TW6180.
Length = 61

Score = 39.1 bits (89), Expect = 0.002
Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + R++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMASRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68063|Y68063|Kunitz protease inhibitor variant BG031.
Length = 61

Score = 39.1 bits (89), Expect = 0.002
Identities = 18/66 (27%), Positives = 33/66 (49%), Gaps = 11/66 (16%)

Query: 28 KIAEKICGDLKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIER 87
++ ++C + +P G C + R++++ T +C F + GC GN NNF +
Sbjct: 1 EVVREVCSEQAEP-----GPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNF----DT 49

Query: 88 EVACVA 93
E C+A
Sbjct: 50 EEYCMA 55

>GSP:Y68064|Y68064|Kunitz protease inhibitor variant BG032.
Length = 61

Score = 39.1 bits (89), Expect = 0.002
Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + R++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68105|Y68105|Kunitz protease inhibitor variant TW6157.
Length = 61

Score = 39.1 bits (89), Expect = 0.002
Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + R++++ T +C F + GC+GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68109|Y68109|Kunitz protease inhibitor variant DD101.
Length = 61

Score = 39.1 bits (89), Expect = 0.002
Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + R++++ T +C F + GC+GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCDGNRNNF----DTEEYCMA 55

>GSP:Y68139|Y68139|Kunitz protease inhibitor variant BG003.
Length = 61

Score = 39.1 bits (89), Expect = 0.002
Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYNNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
+++ C G C + R++++ T +C F + GC GN NNF + E C+A
Sbjct: 3 VREVCSEQAETGPCRAMLRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68143|Y68143|Kunitz protease inhibitor variant TW6189.
Length = 61

Score = 39.1 bits (89), Expect = 0.002
Identities = 17/57 (29%), Positives = 30/57 (51%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIERYEVACVA 93
 +++ C G C + +R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAMIWRWYFDVTEGKCAPFFYGGCYGNRNNF----DTEEYCMA 55

>GSP:Y68151|Y68151|Kunitz protease inhibitor variant DD131.
 Length = 61

Score = 39.1 bits (89), Expect = 0.002
 Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIERYEVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRALFKRWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68166|Y68166|Kunitz protease inhibitor variant BG029.
 Length = 61

Score = 39.1 bits (89), Expect = 0.002
 Identities = 16/57 (28%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIERYEVACVA 93
 +++ C G C + + +++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68181|Y68181|Yeast mating-factor and KPI-P48 protein sequence
 Fig 26.
 Length = 146

Score = 39.1 bits (89), Expect = 0.002
 Identities = 16/57 (28%), Positives = 28/57 (49%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIERYEVACVA 93
 +++ C G C + + +++++ T +C F + GC GN NNF + E C+A
 Sbjct: 88 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEXCMA 140

>GSP:Y68182|Y68182|KPI-P48 protein sequence Fig 42.
 Length = 61

Score = 39.1 bits (89), Expect = 0.002
 Identities = 16/57 (28%), Positives = 28/57 (49%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIERYEVACVA 93
 +++ C G C + + +++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEXCMA 55

>GSP:Y68157|Y68157|Kunitz protease inhibitor variant BG015.
 Length = 61

Score = 38.7 bits (88), Expect = 0.003
 Identities = 16/57 (28%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIERYEVACVA 93
 +++ C G C + + +++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAETGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>GSP:Y68167|Y68167|Kunitz protease inhibitor variant BG030.
 Length = 61

Score = 38.7 bits (88), Expect = 0.003
 Identities = 16/57 (28%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIERYEVACVA 93
 +++ C G C + + +++++ T +C F + GC GN NNF + E C+A
 Sbjct: 3 VREVCSEQAESGPCRALIYHWYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 55

>PIR:A32761|A32761|hypothetical Alzheimer's disease amyloid beta
 protein, Alu-containing clone - human (fragment)
 >STR:Q13793|Q13793|AMYLOID PROTEIN (FRAGMENT).
 >GNP:M28373|M28373_1|Homo sapiens amyloid protein A4
 precursor mRNA, 3' end of cds.

Length = 484

Score = 38.7 bits (88), Expect = 0.003

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 208 VREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 260

>STR:Q13764|Q13764|AMYLOID-BETA PROTEIN. >GNP:M34875|M34875_1|Human
 amyloid-beta protein (APP) gene, exon 13; alternate
 amyloid-beta protein.
 Length = 547

Score = 38.7 bits (88), Expect = 0.003

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 287 VREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 339

>RTR:CAA02049|CAA02049|APP PRECURSOR PROTEIN (FRAGMENT).
 >GNP:A31584|A31584_1|H.sapiens APP precursor gene.
 Length = 770

Score = 38.7 bits (88), Expect = 0.003

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 287 VREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 339

>GNP:X06981|X06981_1|Human mRNA fragment for amyloid beta-protein
 (AP) insertion; amyloid protein precursor (AA 289-364;
 81AA).
 Length = 81

Score = 38.7 bits (88), Expect = 0.003

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 1 VREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 53

>GNP:X06982|X06982_1|Human mRNA fragment for amyloid beta-protein
 (protease inhibitor domain); amyloid protein precursor
 (62 AA).
 Length = 62

Score = 38.7 bits (88), Expect = 0.003

Identities = 17/57 (29%), Positives = 29/57 (50%), Gaps = 4/57 (7%)

Query: 37 LKDPCKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVA 93
 +++ C G C + R++++ T +C F + GC GN NNF + E C+A
 Sbjct: 2 VREVCSEQAETGPCRAMISRWFYFDVTEGKCAPFFYGGCGGNRNNF----DTEEYCMA 54

>GSP:W30063|W30063|EST R74593 protein.
 Length = 169

Score = 33.6 bits (75), Expect = 0.090

Identities = 13/58 (22%), Positives = 27/58 (46%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETFFVSGCNGNLNNFKLKIEREVACVAKYKPP 98
 C + G C R++++ C F++ GC GN N+++ + + C + + P
 Sbjct: 58 CTANAVTGPCRASFPWRWFYFDVERNSCNNFIYGGCRGNKNSYRSEEACMLRCFRQENP 115

>GSP:W30049|W30049|Human placental bikunin.
 Length = 58

Score = 33.2 bits (74), Expect = 0.12

Identities = 14/54 (25%), Positives = 26/54 (47%), Gaps = 4/54 (7%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAK 94
 C + G C R++++ C F++ GC GN N+++ E AC+ +
 Sbjct: 5 CTANAVTGPCRASFPFRWYFDVERNSCNNFIYGGCRGNKNSYR----SEEACMLR 54

>GSP:W30050|W30050|Human placental bikunin.
 Length = 51

Score = 33.2 bits (74), Expect = 0.12
 Identities = 14/54 (25%), Positives = 26/54 (47%), Gaps = 4/54 (7%)

Query: 41 CKLDMNFGSCYEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAK 94
 C + G C R++++ C F++ GC GN N+++ E AC+ +
 Sbjct: 1 CTANAVTGPCRASFPFRWYFDVERNSCNNFIYGGCRGNKNSYR----SEEACMLR 50

>SP:P52788 O00544|SPSY_HUMAN|SPERMINE SYNTHASE (EC 2.5.1.22)
 (SPERMIDINE AMINOPROPYLTRANSFERASE) (SPMSY).
 >GNP:AD001528|AD001528_1|Homo sapiens spermidine
 aminopropyltransferase mRNA, complete cds; spermine
 synthase.
 Length = 366

Score = 27.0 bits (58), Expect = 8.9
 Identities = 12/36 (33%), Positives = 19/36 (52%), Gaps = 5/36 (13%)

Query: 18 LNTLLLGGVNKKIAEKICGDLKDPCKLDMNFGSCYEV 53
 ++ +++ G K K CGD+ D K G CY+V
 Sbjct: 221 IDQMVIDGCKKYMRKTCGDVLDNLK-----GDCYQV 251

>PIR:S54160|S54160|spermine synthase (EC 2.5.1.22) - human
 >GNP:Z49099|Z49099_1|H.sapiens mRNA for spermine
 synthase; spermidine aminopropyltransferase.
 Length = 368

Score = 27.0 bits (58), Expect = 8.9
 Identities = 12/36 (33%), Positives = 19/36 (52%), Gaps = 5/36 (13%)

Query: 18 LNTLLLGGVNKKIAEKICGDLKDPCKLDMNFGSCYEV 53
 ++ +++ G K K CGD+ D K G CY+V
 Sbjct: 223 IDQMVIDGCKKYMRKTCGDVLDNLK-----GDCYQV 253

>STR:Q9UQS1|Q9UQS1|SPERMIDINE AMINOPROPYLTRANSFERASE (FRAGMENT).
 >GNP:U53331|U53331_1|Homo sapiens cosmid clone U129A10
 from Xp22.1-22.2, complete sequence; match to AD001528
 (PID:g2198557), but note unusual splice at 19806 and
 20569; H_U129A10.1.
 Length = 349

Score = 27.0 bits (58), Expect = 8.9
 Identities = 12/36 (33%), Positives = 19/36 (52%), Gaps = 5/36 (13%)

Query: 18 LNTLLLGGVNKKIAEKICGDLKDPCKLDMNFGSCYEV 53
 ++ +++ G K K CGD+ D K G CY+V
 Sbjct: 204 IDQMVIDGCKKYMRKTCGDVLDNLK-----GDCYQV 234

>RTR:BAA20005|BAA20005|5'OY11.1 PROTEIN (FRAGMENT).
 >GNP:D87009|D87009_3|Homo sapiens immunoglobulin lambda
 gene locus DNA, clone:288A10; putative.
 Length = 541

Score = 27.0 bits (58), Expect = 8.9
 Identities = 13/49 (26%), Positives = 23/49 (46%), Gaps = 5/49 (10%)

Query: 51 YEVHFRYFYFNRTSKRCETVFVSGCNGNLNNFKLKIEREVACVAKYKPPR 99
 Y H+R + +++ +C S C FK K+E + C +K P+
 Sbjct: 445 YMCHYRGHWGKSAHQ-----SKRLQLFLTFKEKMEHKTQCHQMFKKPK 488

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens
 Posted date: Oct 5, 2000 10:09 AM
 Number of letters in database: 24,820,038
 Number of sequences in database: 113,759